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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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2 US-08-439-814-3

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2 US-08-439-814-1

2 US-08-39-814-1

2 US-08-39-814-1

2 US-09-949-016-70890

4 US-09-949-016-14186

1 US-09-621-976-17501

1 US-09-621-976-17501

1 US-09-621-976-17503

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     Sequence
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2, Appli
70889, A
70889, A
70889, A
13840, Appl
13840, A
17500, A
17501, A
17502, A
13989, A
13989, A
12422, A
12422, A
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67.5	67.5	67.5	67.5	67.5	67.5	67.5	69.2	69.2	69.2	69.2	69.2	69.2	69.2	69.2	69.2	69.2	69.2
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US-09-949-016-14445	US-09-949-016-12569	US-09-949-016-15728	US-09-184-418C-3	US-09-184-418C-29	US-09-308-080-1	US-09-308-080-7	US-09-643-990A-1	US-09-557-884-1	US-09-949-016-12106	US-09-949-016-17037	US-09-949-016-16061	US-09-949-016-12614	US-09-949-016-12474	US-09-949-016-13693	US-09-949-016-17275	US-09-949-016-12335	US-09-949-016-17054
Sequence 14445, A	sequence 12569, A			Sequence 29, Appi		Sequence /, Appri	ຸ	Sequence I, Appli	Sequence 12106, A								-

ALIGNMENTS

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Patent No. 5968735
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE P 4238778.7
PILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE PCT/DE93/01086
PILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
APPLICATION NUMBER: WO PC
FILING DATE: 10-NOV-1993
.NFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ
                                                                                          COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 12-MAY-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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LENGTH: 568 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 655 Fifteenth Street, N. W., Suite 330 G STREET: Street Lobby CITY: Washington STATE: DC
                                                                                                                                                                                                                                                        TELEPHONE: 202/638-500
TELEPAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 100.0%; Score 24; DB Local Similarity 100.0%; Pred. No. 0.02 nes 24; Conservative 0; Mismatches
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STRANDEDNESS: single
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                                                          WO PCT/DE93/01086
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RESULT 3
US-08-439-814-2/c
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                                                                                         APPLICATION NUMBER: WO FILING DATE: 10-NOV-19 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
PILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P161
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1942
PRIOR ADDITORIOR 12-NOV-1942
                                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: STEIN, CALLING APPLICANT: WALTHER, WOITGANG THE EXPRESSION OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIKAIDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 655 FILE
STREET: Street Lobby
CITY: Washington
                                   STRANDEDNESS: single
   IOPOLOGY: ]
                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y Match 100.0%; Score 24; I Local Similarity 100.0%; Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         953 CTTATGTAGACACGTCTTTCAAAG 930
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                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP 655 Fifteenth Street, N. W., Suite 330 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                     linear
                                                                                                             10-NOV-1993
EQ ID NO: 2:
DNA (genomic)
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                                                                                                                                                  WO PCT/DE93/01086
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                                                         US-08-439-814-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08439814
Patent No. 5968735
GENERAL INFORMATION:
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Best Local Similarity
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: 91614-5015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STEIN, ULTIKE
APPLICANT: WALTHER, WOLFGANG
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202/638-5000
TELEPAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                            APPLICATION NUMBER: DE PA
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PO
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30B PRIOR APPLICATION DATA:
                                                                           MOLECULE TYPE:
                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                             TOPOLOGY:
                                                                                                             STRANDEDNESS: single
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                                                                                                                                 nucleic acid
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                                                                                               linear
                                                                         DNA (genomic)
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 100.0%;
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Pred. No. 0.032;
 Score 24; DB 2;
Pred. No. 0.033;
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                   Length 2090;
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; ORGANISM: Human
US-09-949-016-70889
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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US-09-949-016-70890/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70889
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
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                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 70890
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Best Local Similarity
                                                                     Best Local Similarity
Matches 19; Conserv
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                                                                                                        Query Match
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: CL001307
                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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 TTATGTATACATGTCTTTTAAA 74
                                    TTATGTAGACACGTCTTTCAAA 23
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86.4%;
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                                                                         Score 17.2; D
Pred. No. 61;
0; Mismatches
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Pred. No. 6
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
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                                                                                                                                                                                           Sequence 14186, Appearent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.7%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Lander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/054,272
FILING DATE: 01-APR-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cargill, Michele
APPLICANT: Ireland, James S
APPLICANT: Rozen, Steven G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 781-861-9540
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SOFTWARE: FastSE(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                   4230 CTAATGTAGACAGCTCTTTCAA 4251
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Daley, George Q.
Cargill, Michele
Ireland, James S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                Application US/09949016
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SYSTEM: Windows 95
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SEQ ID NO 13840

LENGTH: 276687

TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(27667)
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; ORGANISM: Human
US-09-949-016-14186
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APPLICANT: VENTER, J.
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Best Local (
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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
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Matches 19; Conserv
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SEQ ID NO 14186
LENGTH: 125536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-90-08
NUMBER OF SEQ ID NOS: 207012
SOFTMARE: FASEISEQ for Windows Version 4.0
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20
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PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
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86.4%;
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Pred. No. 1.
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Pred. No. 1.
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOPTWARE: Patent.pm
SEQ ID NO 17501
LENGTH: 103
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17501
                                                                                                                                                                APPLICANT: Dumas wilne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17503
LENGTH: 126
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; ORGANISM: Homo sapiens
US-09-621-976-17500
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US-09-621-976-17501/c
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US-09-621-976-17503/c
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Patent No. 6639063
GENERAL INFORMATION:
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Best Local Similarity
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Matches 17; Conserv
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Best Local :
                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
-09-621-976-17503
                                                             Matches
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17; Conserv
                              1 CTTATGTAGACACGTCT 17
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   CTTATGTAGACACGTCT 58
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Sequence 11249, Application US/09621976

Patent No. 6639063

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JOBert, S.
APPLICANT: Giordano, J.Y.
ITILE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens US-09-621-976-17502
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US-09-621-976-13989/c
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US-09-621-976-11249/c
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTB and Encoded Human Proteins.
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SEQ ID NO 17502
LENGTH: 137
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: PAtent.pm
SEQ ID NO 13989
LENGTH: 150
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Patent No. 6639063
GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11249
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APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
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Local Similarity 100.0%; Pred. No.
1es 17; Conservative 0; Mismatc
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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24
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9C_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USO9B_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOB_PUBCOMB.seq:*
/ Cgn2_6/ptodata/1/pubpna/USOC_PUBCOMB.seq:*
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539.601 Million cell updates/sec
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. 6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	당성	r		ID	Description
c :	24	100.0	:	18	US-10-482-433A-3	Sequence 3, Appli
ი 2	24	100.0		18	US-10-473-126-37	Sequence 37, Appl
c u	19.8	82.5		18	US-10-482-433A-6	Sequence 6, Appli
Ω 4	19.8	82.5		17	US-10-451-646-24	Sequence 24, Appl
ი თ	19:8	82.5		18	US-10-473-126-167	Sequence 167, App
σ	18.2	75.8	491	18	US-10-437-963-86300	Sequence 86300, A
c 7	18.2	75.8		10	US-09-770-961-577	Sequence 577, App
8	18.2	75.8		18	US-10-357-930-19156	Sequence 19156, A
ი 9	18.2	75.8		18	US-10-357-930-54995	Sequence 54995, A
10	18.2	75.8		18	US-10-357-930-48960	Sequence 48960, A
11	18.2	75.8		18	US-10-437-963-86301	Sequence 86301, A

RESULT 2 US-10-473-126-37/c

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16.8 16.8	17.2 17.2 17.2 17.2			17.8 17.8 17.8 17.8 17.8 17.8 17.6 17.6 17.6	18.2 18.2
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-637	US-10-282-122A-183U4 US-09-764-872-700 US-10-719-993-6811 US-10-097-111-10 US-09-864-761-6452	-10	US-10-027-632-274931 US-10-027-632-274932 US-10-027-632-274931 US-10-027-632-274932	US-10-027-632-8632 US-10-027-632-8632 US-10-027-632-99405 US-10-027-632-99406 US-10-027-632-99406 US-10-027-632-99406 US-10-027-632-99406 US-10-027-632-99406 US-10-027-632-99406 US-10-719-993-6890 US-09-814-353-5727 US-09-814-353-12011 US-10-357-930-50147 US-10-357-930-50147 US-10-382-1228-38309 US-10-741-601-19969 US-10-741-601-5694 US-10-098-263B-45459 US-10-098-263B-45459 US-10-098-263B-45459 US-10-098-263B-45459 US-10-674-124A-13252	73-126 73-126
e 398, e 2147 e 2147	Sequence 100, App Sequence 700, App Sequence 6811, Ap Sequence 10, Appl Sequence 6452, Ap		Sequence 274931, Sequence 274932, Sequence 274931, Sequence 274932,		168, A

ALIGNMENTS

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RESULT 4

US-10-451-646-24/c
US-10-451-646-24/c
US-10-451-646-24/c
Sequence 24, Application US/10451646
; Publication No. US20040067508A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
Method for the Simultaneous Amplification of Multiple
TITLE OF INVENTION: Sequences in a PCR Reaction and Marking Thereof
FILE REFERENCE: PCT/DE 01/04951
; FILE REFERENCE: PCT/DE 01/04951
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US-10-482-433A-6
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            SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
LENGTH: 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/482,433A CURRENT FILING DATE: 2003-12-29 PRIOR APPLICATION NUMBER: DE 10132212.7 PRIOR FILING DATE: 2001-06-27 NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin version 3.2 SEQ ID NO 6 TENERTH: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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LENGTH: 2932
TYPE: DNA
CRGANISM: Homo Sapiens
                                                                       CURRENT APPLICATION NUMBER: US/10/451,646
CURRENT FILING DATE: 2003-06-23
NUMBER OF SEQ ID NOS: 25
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative TITLE OF INVENTION: analysis of single strands of amplificates FILE REFERENCE: 82174
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Epigenomics AG
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CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No. 23;
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Pred. No. 0.
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RESULT 5
US-10-473-126-167/c
; Sequence 167, Appli
; Publication No. US;
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85354C.1 US-10-437-963-86300
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                                                                                                             APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT FILING DATE: 2003-05-14 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 86300 LENGTH: 491 TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 167
LENGTH: 2932
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86300, Application US/10437963 
Publication No. US20040123343A1
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Best Local Similarity
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
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Best Local Similarity
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                                     FEATURE:
NAME/KEY: unsure
LOCATION: (1)...(491)
OTHER INFORMATION: unsure at
                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                              FEATURE:
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Wu, Wei
                                                                                                                                                                                                                                                                                                     Boukharov, Andrey A.
Barbazuk, Brad
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ilarity 91.3%;
Conservative
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; Pred. No. 29;
0; Mismatches
                                              all n locations
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APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neith
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of A
TITLE OF INVENTION: Expressed Sequences of A
TITLE OF INVENTION: Under US/09/770,961
CURRENT APPLICATION NUMBER: US/09/770,961
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR APPLICATION NUMBER: 60/178,466
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 577
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US-10-357-930-19156
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; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-961-577
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Best Local (
                                                                                                                                                                                   Sequence 19156, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION:
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                APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gorlach, Jorn
PRIOR APPLICATION NUMBER: 09/785,276
                                                                                                                                                                                                                                                                                                                               297
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Similarity 87.0%;
20; Conservative
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                                                                                                                                                                                                                                                                                                                               TTATGTAGACAAGTATGTCAAAG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu, Yang
<sup>Tameaka</sup>, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Davis, Keith
Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Garcia, Carlos A.
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Haas, William David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matthew, Abraham V.
Ledford, Brooke L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raines, Tracy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09770961
o. US20030115639A1
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Slader, Ted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Keith R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>
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Pred. No. 1.3e+02;
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PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR PPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-07-18
PRIOR PILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: PASCSEQ for Windows Version 4.0
SEQ ID NO 54995
LENGTH: 597
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: 166, 171
; OTHER INFORMATION: n = A,T,C
US-10-357-930-19156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-10-357-930-54995/c
US-10-357-930-54995, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
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                                                                                                  ; ORGANISM: Homo sapiens 
US-10-357-930-54995
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PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
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NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 19156
LENGTH: 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
Query Match 75.8%;
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
ERIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: MONAHAN, JOHN
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MRI-007BCN
TILE REFERENCE: MRI-007BCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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87.0%;
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  Score 18.2; DB 18;
Pred. No. 1.3e+02;
0; Mismatches 3;
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Pred. No. 1.3e+02;
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                                                  Length 597;
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Gaps

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142

CTTATGTAGACACGTCTTTCAAA

23

CTTATGGAGATATGTCTTTCAAA 120

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Sequence 48960, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
ITITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KI
ITITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MEI-007BCN
FILE REFERENCE: MEI-007BCN
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-357-930-48960
SEQ ID NO 86301
LENGTH: 1504
                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LA ROBA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/189,862
PRIOR FILLING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILLING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/211,314
PRIOR FILLING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/219,007
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR APPLICATION NUMBER: 60/255,281
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                                      TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT:
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CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 09/785,276
PRIOR FILING DATE: 2003-02-16
PRIOR FILING DATE: 2003-02-16
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PRIOR FILING DATE: 2000-02-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
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Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCATGTAGACTCTTCTTTCAAA 394
                                                                                                                                                                                       Barbazuk, Brad
                                                                                                                                                                                                                Boukharov, Andrey A.
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87.0%;
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Pred. No. 1.3e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 642;
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SEQ ID NO 168
LENGTH: 2932
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-10-473-126-313/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: chemically treated genomic DNA (Homo US-10-473-126-168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85355C.1
US-10-437-963-86301
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APPLICANT: Epigenomics AG
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
                                                                                                                                                                                                  SEQ ID NO 313
LENGTH: 2932
                                                             Matches
                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                              Sequence 313, Application US/10473126 Publication No. US20040234973A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                  FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
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TITLE OF INVENTION: Methods and nucleic acids
TITLE OF INVENTION: proliferative disorders
                                                                                                                                   OTHER INFORMATION: chemically treated genomic
                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                        TYPE: DNA
                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 75.8%;
Local Similarity 87.0%;
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828
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                                                           20;
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20; Conserv
                                                                          Similarity
                     CTTATGTAGACACGTCTTTCAAA 23
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                          75.8%;
87.0%;
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Pred. No. 1.7e+02;
0; Mismatches 3;
                                                                       Score 18.2;
Pred. No. 1
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Pred. No. 1
                                                          Mismatches
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                                                                         .7e+02
                                                                                      DB 18;
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                                                                                                                                   (Homo sapiens)
                                                                                    Length 2932;
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US-10-027-632-8632
Sequence 8632, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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; ORGANISM: Human
US-10-027-632-8632
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1000-11-21
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US-10-027-632-8632
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-8632
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PRIOR FILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRIOR PRIOR DATE: 1999-09-28
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Best Local &
                                                                                    SOFTWARE: FastSEQ
SEQ ID NO 8632
LENGTH: 619
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APPLICANT: Wang, David G.
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8632, Application US/10027632 Publication No. US20030204075A9
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Aad38998 Human mdr
Aag62615 Human mdr
Abx94595 Human mdr
Aag62614 Human mdr
Aag62612 Human mdr
Aag62612 Human mdr
Aag62615 Human 5'
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77.5	77.5	77.5	77.5	77.5	77.5	77.5	77.5		77.5	77.5	78.3	79.2	79.2	82.5	82.5	82.5	82.5	82.5	82.5	83.3	87.5	87.5	91.7	91.7
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ALIGNMENTS

RESULT 1 AAD39008/c

AAD39008 standard;

DNA; 24

AAD39008;

23-SEP-2002 (first entry)

Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; ds. Human mdr1 gene HIF-1 binding site DNA #1 02-MAY-2002. misc_binding Homo sapiens. Colgan SP; 26-OCT-2000; 2000US-0243542P 25-OCT-2001; WO200234291-A2 (BGHM) BRIGHAM & WOMENS HOSPITAL INC. 2001WO-US049856 Location/Qualifiers
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ADB20870 ADB87959 ADB96942 ADB92133

Abs98184 Human mul
Aad41243 Human MDR
Acf62751 Cancer ba
Adb20870 MRP1 base
Adb87959 Human UGT
Adb96942 Human MDR
Adb92031 Human MDR
Aad39037 Human mdr
Aad39033 Human mdr

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

binding molecules.

WPI; 2002-471427/50.

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Example

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Page 12; 92pp;

English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC The invention relates to a method of treating a subject having or at risk C of developing a haematologic malignancy or multidrug resistance (MDR). CC The method involves administering hypoxia inducible factor-1 (HIF-1) complex modulators. Modulation molecules or small ubiquitin-like-modifier (SUMO)-1 binding molecules or antisense mucleic acid molecules and CC subject having molecules or antisense mucleic acid molecules and CC subject having or at risk of developing haematologic malignancy or MDR CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoma, myeloma or chronic lymphoproliferative disorders include chronic or acute myeloid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia, e.g. angiogenic myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The came HIF-1 hinding aire nan
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/note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                            backbone; ss.
                                                                                                                     WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; I
Pred. No. 0.
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   ubiquitin-like-modifier-1
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This is a preferred fragment of the mdr-1 gene promoter, isolated human DNA. The mdr-1 promoter and enhancer elements are inducible cytostatic agents such as vincristine and adriamycin which are use cancer therapy. Vectors comprising the promoter and enhancer seque

lucible by are used in

from

Claim 2; Page 6; 7pp;

German

cytostatic

agents.

WPI; 1994-168680/21.

New mammalian expression vector useful for gene therapy, - comprisi promoter and/or the enhancer of the mdr-1 gene which is susceptible

comprising the sceptible to

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RESULT 3
AAQ62615/c
ID AAQ626
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CX Induci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method of treating a subject having or at risk CC of developing a haematologic malignancy or multidrug resistance (MDR). CC The method involves administering hypoxia inducible factor-1 (HIF-1) CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding CC molecules or small ubiquitin-like-modifier (SUMO)-1 binding CC element (HRE) binding molecules or antisense mucleic acid molecules and CC (SUMO-1 binding molecules or antisense molecules are useful for treating a CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders include lymphocytic leukaemia or chronic lymphoproliferative disorders CC e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid CC disorders include chronic or acute myeloid leukaemia, e.g. angiogenic CC invention is used in gene therapy. The present sequence is an antisense CC oligo targetted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its CC expression. This oligo is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inducible promoter; cytostatic agent; adriamycin; vincristine;
multiple drug resistance; mdr-1; mammalian expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DE4238778-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                 (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mdr-1 promoter fragment.
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17-JAN-1995
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Similarity 100.0%;
24; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                               Walther
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Pred. No.
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This invention describes a novel method of determining cytosine CC methylation in a sample of genomic DNA which comprises treating the CC sample with hydrogen sulphite so that the cytosine is converted to uracil CC whilst 5-methylcytosine remains unchanged, amplifying sections of the DNA CC using at least 2 PCR primers and studying the base composition of both CC complementary amplified strands whereby methylation status is deduced CC from the difference in molecular weight of the two strands. The method is CC used to diagnose and/or prognose unwanted side effects of medication, CC cancer, central nervous system disorders, aggression symptoms or CC cancer, central nervous system disorders, aggression symptoms or CC behavioural disorders, clinical, psychological and social consequence of Drain damage, psychotic and personality disorders, dementia and CC associated disorders, cardiovascular disease, malfunction, damage or CC disease of the gastrointestinal tract, breathing system, bone muscle, cendocrine or metabolic system, injury, infection, abnormal development or Sexual malfunction. This sequence represents the human MdrI DNA fragment CC amplified by the PCR primers represented in ABX94593 & ABX94594 and is CC used to illustrate the method of the invention
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MdrI; cytosine methylation; hydrogen sulphite; diagnose; dementia; 5-methylcytosine; amplification; prognose; side effect; medication; bone; cancer; central nervous system disorder; aggression; muscle; endocrine; abnormal development; personality disorder; behavioural disorder; injury; brain damage; psychotic disorder; cardiovascular disease; infection; gastrointestinal tract; sexual malfunction; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 17; 38pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining cytosine methylation in a genomic DNA sample by treating hydrogen sulfite and analyzing the result, to diagnose associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-201513/19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cancer and
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local ?
                                                                                                        This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 633 BP; 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ62614;
                                                                                                                                                                                                                                          New mammalian expression vector useful for gene therapy, - comprising promoter and/or the enhancer of the mdr-1 gene which is susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inducible promoter; cytostatic agent; adriamycin; vincristine; multiple drug resistance; mdr-1; mammalian expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ62614
                                                                        Sequence 1318
                                                                                                                                                                                                                               cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                               DE4238778-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human mdr-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
17-JAN-1995
                                                                                                       interferon, IL-2, IL-6, etc.) can be excontrol of cytostatic agents. (Updated
                                                                                                                                                                                                                                                                                                                                              12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1994
                                                                                                                                                                                                                                                                                                                        (DELB-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                         DELBRUECK CENT
                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTATGTAGACACGTCTTTCAAAG
CTTATGTAGACACGTCTTTCAAAG
                                                                                                                                                                                                         Page 5;
                                                                                                                                                                                                                                agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                            100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
                                                                       BP; 430 A; 237 C; 277
                                                                                                                                                                                                                                                                                                                                              92DE-04238778
                                                                                                                                                                                                                                                                                                                                                                    92DE-04238778
                                                                                                                                                                                                        7pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 143 C; 165 G; 164 T; 0 U; 0 Other;
                                                                                                                                                                                                           German.
                                                                                                                                                                                                                                                                                                                         MOLEKULARE MEDIZIN MAX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                               0
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Pred.
                                          Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188
         24
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                                                                          <u>ი</u>
                                                                           374 T; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.12;
                                         0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                     BB
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                                                    Length 1318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                Indels
                                                                           0 Other;
                                                                                                                                                                                                                                                       comprising
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RESULT 7
AAQ62612/c
ID AAQ62612 standard; DNA; 2090 BP
XX
AC AAQ62612;
XX
DT 25-MAR-2003 (revised)
DT 17-JAN-1995 (first entry)
XX
DE Human mdr-1 promoter fragment.
XX
Inducible promoter; cytostatic
XX
KW multiple drug resistance; mdr-1
XX
OS Homo sapiens.
XX
OS Homo sapiens.
XX
DE4238778-A1.
                                                                                                                                                                                                                                                                                                                            5
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                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, II-2, II-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
                                                                       inducible promoter; cytostatic agent; adriamycin; vincristine;
multiple drug resistance; mdr-1; mammalian expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1688 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 5; 7pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytostatic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New mammalian expression vector useful for gene therapy, - comprising the promoter and/or the enhancer of the mdr-1 gene which is susceptible to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-168680/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inducible promoter; cytostatic agent; adriamycin; vincristine;
multiple drug resistance; mdr-1; mammalian expression vector;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human mdr-1 promoter fragment
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17-JAN-1995
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                                                                                                                                                                                                                                                                                                   1323
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                  CTTATGTAGACACGTCTTTCAAAG 1300
                                                                                                                                                                                                                                                                                                                   CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Walther W;
                                                                                                                       promoter fragment.
                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first en
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                                                                                                                                                                                                                                                                                                                                                                                                                 556 A; 311 C; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 24; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                450 T;
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                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                   Length 1688;
                                                                                                                                                                                                                                                                                                                                                                                                                U; 0 Other;
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RESULT 8
ABZ09897/
ID ABZ0
XX ABZ0
AC ABZ0
XX Huma
XX Huma
XX Gene
KW Gytc
XX Homa
KW Gone
KW WO20
AX HOMA
AX HOMA
XX LEPI
PI GENI
PI Lewi
PI Schwi
XX WPI
XX WPI

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Best Local
                                    Olek A, Pic
Lewin A, L:
Schwope I,
                                                                                                                                                                                                                                                     Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaem cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                        9897/c
ABZ09897
                                                                          Berlin K,
                                                                                                                            26-MAR-2001; 2001US-0278333P
                                                                                                                                                      26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                ABZ09897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                        WO200277272-A2
                                                                                                                                                                                                                                                                                                           Human 5' and/or regulatory region of MDR1 DNA SEQ ID NO:37.
                                                                                                                                                                                                                                                                                                                                      16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2090 BP; 714 A; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in
                                                                                                    (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian expression vector promoter and/or the enhancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Page 4; 7pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                   Piepenbrock C, Adorjan
, Lipscher E, Maier S,
I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTATGTAGACACGTCTTTCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTATGTAGACACGTCTTTCAAAG 1702
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                                                                          Braun A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                       DNA; 2932
                                                                                                    AG.
                                                                       Distler J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 444 G; 567 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; DB 2
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                               Guetig D,
P, Grabs (
Model F, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for gene therapy, - comprisir the mdr-1 gene which is susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
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                                               G, Lesche R, Leu
Mueller V, Otto T,
                                                                                                                                                                                                                                                                     myelogenous leukaemia;
                                                                          Howe A,
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                                                                 Mueller J;
e R. Leu E
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                                                Pelet C;
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WPI; 2003-018942/01

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RESULT 9
ADB53945/c
ID ADB539
XX ADB539
XX ADB539
XX O4-DEC
XX Colon
KW Cytost
XX Uniden
OS Uniden
XX Uniden
XX 27-FEE
XX 27-FEE
XX 27-FEE
XX 1EPIG
XX Adorjs
PI Adorjs
PI Rujan
XX Detect
PT absoci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy hasmatopoletic cells and proliferative disorder hasmatopoletic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cyrosine methylation state and/or single nucleotide polymorphisms (SNPs) of hasmatopoletic cell proliferation disorder related sequences and their complements; and as primers for the amplification of hasmatopoletic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of hasmatopoletic cell proliferative disorders. The present method enables a highly specific classification of hasmatopoletic cell proliferative disorders. The present method enables a highly specific classification of hasmatopoletic cell proliferative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                differentiating between haematopoietic cell passociated with at least 1 gene and/or their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 38; SEQ ID NO 37; 117pp; English.
                                                                                                                                         Adorjan F
Rujan T,
                                                                                                                                                                                                                                                                                                              27-FEB-2003; 2003WO-EP002035
                                                                                                                                                                                                                                                                                                                                                                                                         WO2003072821-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 colon cell proliferative disorder; non methylated CpG dinucleotide; cytostatic; cancer; adenoma; carcinoma; cytosine methylation state;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MDR1 genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB53945;
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Detecting and differentiating between colon cell proliferative disorders associated with a gene or its regulatory regions comprises contacting a target nucleic acid in a biological sample obtained from the subject witle
                                                                                                                                                                                                                                                               27-FEB-2002; 2002EP-00004551
                                                                                                                                                                                                                (EPIG-) EPIGENOMICS
                                                                                                  2003-731620/69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allowing for improved and informed treatment of patients
                                                                                                                                            Schmitt A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes a method for detecting and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;
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G
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                                                                                                                                                                       Maier S,
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                         Becker E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2932;
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       es contacting a the subject with
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ADE84005/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or a series of reagents, where the reagent or series of reagents distinguishes between methylated and non methylated CpG dinucleotides within the target nucleic acid. The molecules of the invention demonstrate cytostatic activity whilst the method may useful for detecting and differentiating between colon cell proliferative disorders, including cancers such as colon adenoma and colon carcinoma. The PNA (peptide nucleic acid)-oligomers are useful as probes for determining cytosine methylation state or single nucleotide polymorphisms. The current sequence is that of the genomic DNA region of the invention. This sequence is not shown within the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 46; SEQ ID NO 1; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a reagent
                                                                                                                                                                                                                                                                                                                                                                                                               methylated CpG dinucleotide; single nucleotide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma; follicular lymphoma; diagnosis; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    taken from Wipoweb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; lymphoid cell proliferative disorder; methylation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5' regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADE84005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE84005
                                                                                     Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                  Burger M,
                                                                                                                                                                                                                                             23-NOV-2001;
28-DEC-2001;
                                                                                                                                                                                                                                                                                         25-NOV-2002; 2002WO-EP013265
                                                                                                                                                                                                                                                                                                                         30-MAY-2003
                                                                                                                                                                                                                                                                                                                                                      WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                               (EPIG-) EPIGENOMICS
                                                                                                                                                     2003-457621/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                828 CTTATGTAGACACGTCTTTCAAAG 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2932 BP; 841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; DNA; 2932
                                                                                                                                                                                   Caldwell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                             2001DE-01057491.
2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region of human gene MDR1.
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                                                                                                                                                                                     Genc
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                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 1
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                     Becker
                                                                                                                                                                                     Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                     Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2932;
                                                                                                                                                                                       Nimmrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least

SEQ

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1; 448pp; English

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RESULT 11
ADS88985/c
ID ADS889
XX ADS889
XX ADS889
XX IS Human
XX Gytost
XX Gytost
XX Homo s
XX Homo s
XX Homo s
YX Predi
PT Gisor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 24
                                                                                                                                 Predicting responsiveness of a subject with breast cell disorder, useful for treating or differentiating breast proliferative disorders comprises analyzing methylation genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                               Foekens J,
Nimmrich I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002; 2002DE-01045779
07-JAN-2003; 2003DE-01000096
17-APR-2003; 2003DE-01017955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2003; 2003WO-EP010881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ds; gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2004035803-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human ABCB1 gene SEQ ID. NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADS88985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADS88985 standard; DNA; 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                  2004-348468/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATGTAGACACGTCTTTCAAAG 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genes.
                                                                                                                                                                                                                                                                                                                                                                   Harbeck N,
Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell proliferative disorder; breast; methylation; therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                   Koenig
Schmitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 24; DB 10
Pred. No. 0.15;
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                                                                                                                                                                                                                                                                                                                                                            Maier S, M
Schmitt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                            Martens
M, Look N
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                                                                                                                                                                                                                                                                                                                                                            MP J
                                                                                                                                                                                           proliferative cell
                                                                                                                                                             pattern
                                                                                                                                                                                                                                                                                                                                                            Model
Marx /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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The invention relates to

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novel method

for

predicting

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responsiveness

Isolated nucleic acid molecules having polymorphisms in known human ge e.g. cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for

WPI; 2002-698522/75

Example 2;

SEQ ID

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RESULT 12
ABS98184/c
ID ABS981
XX Human;
XX Human;
XX Cytoch
XX Cytoch
XX Cytoch
XX Gytoch
XX Gytoch
XX Gytoch
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XX Human;
XX Human;
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XX Gy
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1; cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP45002E1; LTF; adreneryic receptor beta1; ADBR1; aryl hydrocarbon; AHR; MRP3; NR112; aryl hydrocarbon receptor nuclear translocator; ARNT; cathepsin S; CTSS; cyclooxygenase 2; COX2; diazepam binding inhibitor; DBI; haematological; epoxide hydroxylase 2; EPHX2; 5-lipoxygenase activating protein; FLAP; glutathione-S-transferase 12; GST12; histamine-N-methyl transferase; HNMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT; NADPH quinone oxidoreductase 23; UDP-glucuronosyl transferase 2B7; UGT2B7; UDP-glucuronosyl transferase 2B7; urokinase receptor; uPA; multidrug resistance 1; lactotransferain; orphan nuclear receptor; uPA; multidrug resistance i; lactotransferain; orphan nuclear receptor;
                                                                                                                                                                                                                                                                                                                                        28-NOV-2000; 2000US-00724389
                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2001; 2001WO-US044838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multidrug resistance associated protein 3; cancer; prostate; acutylcholine muscarinic receptor; CHMR1; CHMR2; CHMR3; CHMR3; CHMR4; CHMR5; altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic acidity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligoners are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of predicting the responsiveness of a subject with a cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200257410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                               (DNAS-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human multidrug resistance gene promoter B and exons 1-3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-2002
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                                                                                                                                                                                                                                                                               DNA SCI LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTATGTAGACACGTCTTTCAAAG 805
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                                                                                                                                                                                                           Hall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        841 A; 564 C; 653 G; 874 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.15;
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ARBSULT 13
AAD41243/c
ID AAD412
XX AAD412
XX AAD412
XX AAD412
XX AAD412
XX AAD412
XX Human
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC CyrCochrome P450 0/281 (CrP4500/281), autenery Crecycle Recycle (CANNT), catchepsin (ALR), aryl hydrocarbon receptor nuclear translocator (CANNT), catchepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding CC inhibitor (DBI), epoxide hydroxylase 2 (CEPHX2), 5-lipoxygenase activating CC protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl CC transferase (NNMT), (Rallikrein 2) KLKZ, nicotinamide -N-methyl CC (UGT2B4), UDP-glucuronosyl transferase 2B4 (CG (UGT2B4), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B4 (UGT2B4), UDP-glucuronosyl transferase 2B4 (UGT2B4), lactotransferrin (LTP), multidrug resistance associated protein 3 (CG (MRB2), orphan nuclear receptor (NR12), or acetylcholine muscarinic CC (MRB2), orphan nuclear receptor (NR12), or acetylcholine muscarinic CC (MRB2), orphan nuclear receptor (LHRI), CHMR2, CHMR3, CHMR4 or CHMR5) sequence. CC dentifying the genes responsible for specific traits within the genome and eventually CC dentifying the genes responsible for a variety of disorder related CC arises as a result of their e.g., overexpression, constitutive CC and/or treating the disorders. The nucleic acid molecules comprising the polymorphic sequences contained in CYP4501A1, CYP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       문
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to the sequence of an isolated nucleic acid molecule comprising at least one base variation from that of a known human cytochrome P450 A1 (CYP4501A1), cytochrome P450 A2 (CYP4501A2), cytochrome P450 02E1 (CYP45002E1), adrenergic receptor beta1 (ADBR1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder-related traits.
                                                                                                                                                                                                                                              Human; transgenic; reporter constructranscriptional regulatory element; p-glycoprotein; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                         Human MDR1 gene 5' flanking region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD41243 standard; DNA; 10200 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                            10-MAY-2002
                                                                                                              WO200236784-A1
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Page 432-437; 714pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8573 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTATGTAGACACGTCTTTCAAAG 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2739 A; 1422 C; 1705 G; 2707 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                   construct; CYP3A4; cytochrome P450;
element; xenobiotic; steroid; MDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 6;
Pred. No. 0.16;
Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 14
ACF6751/c
ID ACF62751 standard; DNA; 177380 BP
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to generation of non-human transgenic animals comprising a reporter construct for producing a detectable amount of a reporter molecule operably linked to a transcriptional regulatory nucleic acid molecule from the human CYP3A4 gene. The invention also relates to transgenic animal for analysing CYP3A4 cytochrome P450 gene regulation. The non-human mammal of the invention is useful for determining whether a compound is capable of effecting the transcription of a human CYP3A4 gene. It is also useful for determining the effect of a compound such as a xenoblotic or steroid on the regulation of expression of the CYP3A4 gene in a human. The present sequence is 5' flanking region of human (p-glycoprotein) MDR1 gene. This sequence is used as a regulatory element in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-human mammal for determining the effect of a compound on regulation of CYP3A4 gene expression, comprises a reporter construct for producing reporter linked to a transcriptional regulatory nucleic acid from a hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-537301/57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-2000; 2000AU-00001161.
10-MAY-2001; 2001AU-00004901.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-2001; 2001WO-AU001407
                                                                                                                                                                                                                                                                           Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma; cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10200 BP; 3296 A; 1785 C; 1985 G; 3134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 83-92; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liddle C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                           Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.
                                                                                                                                                                                                                                                                                                                                                                           08-OCT-2003 (first entry)
                                                                                                         23-JUL-2001; 2001EP-00117608.
24-MAY-2002; 2002EP-00011710.
                                                                                                                                                      23-JUL-2002; 2002WO-EP008219
                                                                                                                                                                                     20-FEB-2003.
              WPI; 2003-268144/26
                                                                                                                                                                                                                  WO2003013534-A2
                                                                          (EPID-) EPIDAUROS BIOTECHNOLOGIE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9051 CTTATGTAGACACGTCTTTCAAAG 9028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goodwin BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                             Kerb R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 24; DB 6; Length 10200; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULT 15
ADB20870/c
ID ADB208
XX ADB208
XX ADB208
XX irinot
KW irinot
KW lung c
KW varian
KW ds.
XX Uniden
XX U02003
XX U02003
XX 20-FEB
XX 21-FEB
XX 21-FEB
XX 21-FEB
XX 22-FEB
XX 22-FEB
XX 22-FEB
XX 23-JUI
PR 23-JU
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Best Local S
Matches 24
                                                                                                                                                                                                 Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1 polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heinrich G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-JUL-2001; 2001EP-00117608, 24-MAY-2002; 2002EP-00011710.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUL-2002; 2002WO-EP008200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-FEB-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRP1 based cancer related nucleic acid SEQ ID NO:683.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPID-) EPIDAUROS BIOTECHNOLOGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New use of irinotecan for preparation of compositions for treating cancer in subject having genome with variant allele comprising cytochrome p450, subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140580
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2003-354397/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kerb R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; DB 8;
Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 177380;
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The present

describes a method for 683; 100pp; English.

the use of irinotecan

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Disclosure;

SEQ invention

ID NO

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can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human (preferably African or Asian) or a mouse. The present sequence represents a sequence which is used in the exemplification of the present invention.
                                                                                                                                                                                                     its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance protein 1 (MRP1) polynucleotide (II). (I) has cytostatic activity. (I) or its derivative
   Sequence 177380 BP;
   58338 A; 32530 C; 31389 G;
55123 T; 0 U; 0 Other;
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Ś Matches Query Match Best Local Similarity 24; Conservative 100.0%; 0; Score 24; [Pred. No. 0. Mismatches BB . 23; 8 0; Length 177380; Indels 0, Gaps

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REFERENCE AUTHORS TITLE VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AX504306 LOCUS DEFINITION ACCESSION RESULT 2 AX504323/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS S 밁 ORIGIN FEATURES SOURCE Query Match Best Local S Matches 24 JOURNAL ORGANISM 24 bp Ax504306 Ax504306 AX504323 Sequence 26 AX504323 AX504323.1 multiple drug resistance Patent: WO 0234291-A 9 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, I Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 24 • Colgan, S.P. Homo sapiens (human) AX504306.1 Compositions and methods for treating Homo sapiens Homo sapiens Similarity 100.0%; Score 24; DB ilarity 100.0%; Pred. No. 2.2; Conservative 0; Mismatches 26 /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606" Location/Qualifiers GI:23386124 from Patent GI:23386135 (human) 24 bp WO0234291. INC. DB 6; Length 24; DNA DNA hematologic malignancies and (US) 0 Indels linear linear PAT 27-SEP-2002 PAT 27-SEP-2002 0, Gaps 0

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                                                             Distler, J. and Leu, E.

Method for detecting cytosine methylation analysing single strands of amplificates patent: WO 03002760-A 3 09-JAN-2003;
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Stein, U. and Walther, W.
Vector for the expression of therapy-relevant
Patent: US 5968735-A 4 19-OCT-1999;
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Patent: WO 0234291-A 26 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
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organism="synthetic construct"
/mol_type="unassigned DNA"
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1967175
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                                                                                                                                                                                                                                                                                                                                                                                                                        Genomic organization of the human multidrug and origin of P-glycoproteins O. Biol. Chem. 265 (1), 506-514 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 976)
Chen,C.J., Clark,D., Ueda,K., Pastan,I.,
Roninson,I.B.
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Isolation and sequence of the promoter region multidrug-resistance (P-glycoprotein) gene
J. Biol. Chem. 262 (36), 17432-17436 (1987)
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/map="7g21"
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STS
                                                                                                                       Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chromosome 7 STSs (1997)
Unpublished (1997)
Synonyms: PGY1
SDB: SDB:583426
GDB DSEG: PGY1
ConTact: Eric D. Green
Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Bldg. 49, Rm. 2A08, Be
Tel: 3014020201
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Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F.,
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S.,
Leckie,M.P. and Green,E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: egreen@nhgri.nih.gov
Primer A: AACGGAAGCCAGAACATTCC
Primer B: AGGCTTCCTGTGGCAAAGAG
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                                                                                                                                                     This STS was developed from sequence determined by another investigator. See GenBank record: M29423 For additional information about the NHGRI chromosome 7 mapping project, see http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID-92128937].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3014024735
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="PGY1"
253. .432
                                                                         organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                               /clone_lib="Eric D. Green"
∟. .976
                                                                                                                                       ocation/Qualifiers
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Best Local Similarity 100.0%;
Matches 24; Conservative 0
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Stein,U. and Walther,W.
Yector for the expression of therapy-relevant genes
Patent: US 5968735-A 3 19-OCT-1999;
Location/Qualifiers
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AR080194
                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1327)

Madden,M.J., Morrow,C.S., Nakagawa,M., Goldsmith,M.E.,
Fairchild,C.R. and Cowan,K.H.

Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdrl gene in vivo

J. Biol. Chem. 268 (11), 8290-8297 (1993)
                                                                                                                                                                                                                                                                      L07624.1 GI:187500
MDR1 gene; P-glycoprotein; multidrug resistance protein.
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                     HUMMDR1P 1327 bp DNA
Human multidrug resistant P glycoprotein
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                                                                                             Original source text: Homo sapiens 4a) bone marrow DNA.
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253. .272
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                                                                               Location/Qualifiers
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/map="7q21"
/cell_type="leukocyte"
                           /mol_type="genomic DN
/db_xref="taxon:9606"
                                                     organism="Homo sapiens"
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                                                                     Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 2 19-OCT-1999;
Location/Qualifiers
1. 1688
                                                                                                                                                                                                                       AR080193 1688 bp
Sequence 2 from patent US 5968735.
AR080193
                                                                                                                                                                   Unknown.
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                                          /organism="unknown"
/mol_type="unassigned DNA"
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/tissue_lib="lambda Charon
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/function="heat shock element"
1171. .>1171
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/gene="PGY1"
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1041. .1170
/gene="PGY1"
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'bound moiety="unknown"
'function="heat shock element"
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 24; Conservative 0
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                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2117)
Stein, U. and Walther, W.
VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES
Patent: WO 9411522-A 1 26-WAY-1994;
MAX DELBRUECK CT FUER MOLEKULA (DE)
Other publication DE 4238778 940519.
Location/Qualifiers
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Sequence
AR080192
                                                                                                                                                                                                                                                                                                                                                                                        A38669
Sequence 1 from Patent
A38669
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Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 1 19-OCT-1999;
Location/Qualifiers
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l Similarity 100.0%;
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                                                                 /replace="t"
                                                                                           replace="c"
                                                                                                                   cell_type="SARCOMAS"
tissue_type="TUMORS"
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/db_xref="taxon:9606"
/clone="CVS-SW1"
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/mol_type="unassigned DNA"
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from patent US 5968735.
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100.0%; Pred. No. 0.96;
tive 0; Mismatches
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Score 24; DB 6;
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Kohno, K., Sato, S., Uchiumi, T., Takano, H., Kato, S. and Kuwano, M.
Tissue-specific enhancer of the human multidrug-resistance (MDR1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multidrug resistance.
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M57450.1 GI:187470
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                                                                                    Sequence 1 from Patent CQ806551 GI:47111933
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91060578
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
Foekens,J.,
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951. .955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                           2159. .2186
/gene="PGY1"
/note="G00-120-712"
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note="G00-120-712"
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 Harbeck, N.,
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Pred. No. 0.95;
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Koenig, T.,
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 Martens, J., Model, F.,
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                                        Euteleostomi;
                                                                                                                                PAT: 10-MAY-2004
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AX457064/c
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                                                                                                                                                                                                                                                                                                                                          щ
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Sequence 25 from Patent
AX457064
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Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H. Methods and nucleic acids for the analysis of hematopoietic cell proliferative disorders
Patent: WO 02077272-A 37 03-OCT-2002;
                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                          Sequence 37
AX598697
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Mammalia; Eutheria;
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Homo sapiens
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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Primates;
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WO02077272
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Epigenomics AG (DE)
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ORIGIN	FEATURES	TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	RESULT 1 CN813365/c		4 4 4 8 4 0		C 36 37 38	ພູບູບູບ ຜູບູບູນ ຜູບູນ		c c 25 c 27 c 27
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BG440031 BG440031 BG440031 CB669434 CB669534 CN301276 CN306DKQ CR01276 CR24215 CA156945 AQ020267 AQ020267 AQ020267 BF195858 BF195858 BF195858 BF195858 AZ00974 CR343395 CL376034	BZ845681 AI729367 AG044289
BG440031 BB045461 CB669495 CB6699534 BI737199 BX825649 AL39395649 AL39395649 CC248215 CA156945 CA156945 CA156945 CA156945 CK50720267 BZ603334 CK507205 BF195858 BF19586 AZ009978 CC343395 CC1376034	BZ845681 AI729367 AG044289
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                                                                                                                                                                                                                                                                                                                                                                        Sugahara, Y. and Hayashizaki, Y.

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                                                                                                                                                                                                                                               Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itch,M., Konno,H., Okazaki,Y. Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Shiraki,T.,
Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                               Hayashizaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus cDNA clone D93
BB662530
BB662530.1 GI:16496284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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cDNA clone D930005N11 5', mRNA sequence.
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/db_xref="taxon:10090"
                                                                                                                                                                                              Location/Qualifiers
/sex="mixed"
                         clone="D930005N11"
                                                                                                                                    organism="Mus musculus"
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Matches 21
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GSS.
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Spermatophyta; Magnoliophyta; Liliopsida;
Clade; Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                             seq primer: TF
                                                                                                                                                                                                                                                                    Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                 Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                 Bennetzen, J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUGIE79TD ZM_0.6_1.0_KB genomic survey sequence.
                                                                                                                                                                                         Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                 Maize Genomics Consortium
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telaw, C.A., Quackenbush, J.,
                                                                                                                                                                                                         301-838-5843
301-838-0208
                                                                                                                                                                                                                                      Medical Center Drive,
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/clone_lib="ZM_0.6_1.0_KB"
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/rot selected genomic DNA library"
                                                                                                  organism="Zea mays"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                    db_xref="taxon:4577"
                                                                                     strain="B73"
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head" _
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Pred. No. 1.1e+02;
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a; Poales; Poaceae; PACCAD
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Query Match Best Local Similarity

80.0%; 87.5%;

Score 19.2; DB 8; Pred. No. 2.3e+02;

Length 780;

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CC365078/c
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BZ984507/c
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PUGIE79TB ZM 0.6_1.0_KB Z
genomic survey sequence.
BZ984507
BZ984507.1 GI:29219374
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1 (bases 1 to 780)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Whitelaw, C.A., Quackenbush, J., Van Miguel, P., Ma, J. and
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Class: sheared ends
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        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panticoideae; Andropogoneae; Zea.

1 (bases 1 to 816)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                            GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
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/clone=11b="ZM 0.6_1.0 KB"
/clone="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0
CoT selected genomic DNA library"
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mol_type="genomic DNA"

strain="B73"
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Pred. No. 2.3e+02;
0; Mismatches 3;
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Other_GSSs: PUGIE79TD
                                                                                                                                                                                                                                                                                                                         Unpublished (2003)
Other_GSS8: PUIKG34TBB
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 889)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
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Class: sheared ends.
                                                                                                                                                                                                                                                           Tel: 301-838-5843
Fax: 301-838-0208
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/clone=1b="ZM 0.6_1.0 KB"
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CoT selected genomic DNA library"
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/clone lib="ZM_0.6_1.0 KB"
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CoT selected genomic DNA library"
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/strain="B73"
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
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                                                                     EcoRI; 0.6-1.0 kb high
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                                                                                                    464 bp mRNA line eca01-18ms1-f06 Eca01 Eschscholzia californica eca01-18ms1-f06 5', mRNA sequence. CD476851 CD476851.1 GI:31398119
     Eschscholzia californica (California poppy)
Eschscholzia californica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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3', genomic survey semierra
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                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Forbes Building Room 303, Tucson, Tel: 520 626 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza rufipogon
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CL745575.1 GI:50686923
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="UK_
/note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /Lissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:4529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Oryza rufipogon"
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Pred. No. 3.3e
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                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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CH230-125M16.TV CHORI-230 Segment
Rattus.
1 (bases 1 to 627)
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                                                                                              Rattus norvegicus (Norway rat)
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                                                                                                                                                                       CH230-125M16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cwd3@psu.edu or jhl10@psu.edu
The sequence provided is trimmed of vector and low quality regions.
Full sequence and original trace file are available from the Plant
Genome Network website (http://pgn.cornell.edu)
Plate: eca01-18ms1 row: f column: 06
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depamphilis,C., Carlson,J., Ma,H., Tanksley,S., Field,D.,
Leebens-Mack,J., Arrington,J., Zahn,L.M., Kong,H., Ilut,D
Druckensmiller,M., Landherr,L., Hu,Y., Plock,S., Wall,K.,
Chiorean,S., Albert,V., Doyle,J., Frohlich,M., Miller,W.,
Oppenheimer,D., Soltis,D., Soltis,D. and Theiseen,G.
Generation of ESTs from early flower buds of Eschscholzia
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 Mueller Laboratory, Department of Biology, A' State University, University Park, PA 16802, USA Tel: 814 863 6413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: M13F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
Contact: Claude dePamphilis or James Leebens-Mack
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/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
/note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
Site_2: Xhol; Plants were grown in greenhouse at Penn
State from commercially available seeds. Only floral buds
with diameter of 2.5 mm of less were collected. This is a
directionally cloned, non-normalized library. Avg. insert
length: 1702; Primers: M13F and M13R; Antibiotic: 50 ug/ml
Ampicillin; Primary Titer: 7E6 pfu total; Amplified Titer:
1.68211 pfu/ml; Mass Excised Titer: 5.682 total; This
library has been generated by the Floral Genome Project
(FGP). We would like to thank Huck Life Sciences
Consortium for their assistance. The Floral Genome Project
is funded by NSF's Plant Genome Research Program
(DBI-0115684). More information about the project can be
obtained at http://fgp.bio.psu.edu"
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/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="eca01-18m81-f06"
/tissue_type="flower buds <= 2.5mm"</pre>
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90.9%;
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Pred. No. 3.3e+02;
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Clones are derived from the rat BAC library CHORI-230

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

(availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 125 row: M column: 16

Seq primer: T7

Class: BAC ends.
                                                                                                                                                                                                        Oryza rufipogon
Oryza rufipogon
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ephraryota; Viridiplantae; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 632)
1 (bases 1 to 632)
Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
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3', genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Riggs,F., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: CH230-125M16.TJ
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Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                              Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, Tel: 520 626 9595
Fax: 520 621 1259
Email http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                          GSS
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Unpublished (2004)
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                     PCR PRimers
                                                                                                                                                             Contact: Rod A. Wing
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FORWARD: TAA TAC GAC TCA CTA TAG GG
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/clone_lib="CHORI-230 Segment 1"
/clone_Tibe="CHORI-230 Segment 1"
/notee="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pieter de Jong"
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/mol_type="genomic DNA"
/strain="BM/SaNHsd/MCW"
/db_xref="taxon:10116"
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Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rufipogon genomic
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                                                                                                     AZ 85721-0036, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone
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CR_BBa0024M03
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CL720267
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JOURNAL
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Matches 20; Conserv
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               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                     Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tu
Tel: 520 626 9595
Fax: 520 621 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 731)
1 (bases 1 to 731)
1 (bases 1 to 731)
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Plate: 0024 row: M column: 03
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
                                                                                                                                                                                                                                                                     FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0048 row: E column: 12
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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731 bp DNA linear GSS 26-JUL-2004
OR_BBa0048E12.f OR_BBa Oryza rufipogon genomic clone OR_BBa0048E12
5', genomic survev secuence
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Kudrna, D., Muller, C., Hatfield, J.,
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                                                                                                                                                                                                                                                                                                                                                                                      PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGTAGACACGTCTTTCAAAG
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78.3%; ilarity 90.9%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="OR_BBa0024M03"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:4529"
                                                                                       /tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/lab_nost="OR_BBa"
/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: Him
                                                                                                                                                                                   /mol_type="genomic_DN
/db_xref="taxon:4529"
                                                                                                                                                                                                                      /organism="Oryza rufipogon"
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90.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               303, Tucson, AZ 85721-0036, USA
Score 18.8; DB 9;
Pred. No. 3.5e+02;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 18.8; DB 9;
Pred. No. 3.4e+02;
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                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 632;
                                    Length 731;
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                                                                                         Site_2:
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Matches

Indels

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Gaps

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AUTHORS
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CL807004/c
LOCUS
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Best Local
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                                                           AI332619
AI332619.1
EST.
                                                                                                     526 bp mRNA linear EST 13-FEB-1999 qq28a04.x1 Soares NhHMPu S1 Homo sapiens cDNA clone IMAGE:1933806 3' similar to SW:MDP1_RABIT p31429 MICROSOMAL DIPEPTIDASE PRECURSOR 1, mRNA sequence.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                       Homo sapiens
                                                                                                                                                                                                                                                                  3 TATGTAGACACGTCTTTCAAAG 24
                                                                                                                                                                                                                                                                                                                     20;
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FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0020 row: P column: 06
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson,
Tel: 520 626 9595
Fax: 520 621 1259
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Gryza rufipogon
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 765)
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OR CBa0020P06.f OR CBa Oryza
5', genomic survey sequence.
CL807004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Rod A. Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2004)
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                                                                                                                                                                                                                                                                                                                                                                                                  /clone="or_CBa0020F06"
/tlssue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_11b="OR_CBa"
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drk treated 36 hrs before harvest"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DN/
/db_xref="taxon:4529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza rufipogon"
/mol type="genomic DNA"
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                                                                           GI:4069178
                                                                                                                                                                                                                                                                                                                                   78.3%;
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Pred. No. 3.5e
0; Mismatches
                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                DB 9;
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e OR_CBa0020P06
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BH812962/c
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Matches 19
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TITLE
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                                                                                                                                                                                                                            1 (bases 1 to 180)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
Shippence-Indexed Library of Insertion Mutations in the
                                                                                                                                                           Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 bp DNA linear SALK_063510 Arabidopsis thaliana TDNA insertion lin thaliana genomic clone SALK_063510, genomic survey BH812962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                w
                                              10010 N. Torrey Pines Road,
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                               Salk Institute Genomic Analysis Laboratory
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSS
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov .
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1131 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: -40UP from Gibco
High quality sequence stop: 412.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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1 (bases 1 to 526)
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    <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not 1;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19M) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified CDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
                             ecker@salk.edu
    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="pooled human melanocyte, fetal heart, pregnant uterus" /lab_host="DH10B"
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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95.0%;
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Pred. No. 5.3e+02;
0; Mismatches 1;
                                                                                            La Jolla,
    recovered
                                                                                            δ
from
                                                                                         92037, USA
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  the left border of
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BZ290962/c
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Matches :
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Class: TDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 197)

Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

Sequence Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ290962 197 bp DNA linear GSS 24-OCT-: SALK 112237.50.25.x Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK 112237.50.25.x, genomic
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Class: TDN
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                                                                                                                                                                                                                                                                                                                                                                           This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 3' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis Genome
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/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana TDNA insertion lines
/note="DCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elemente. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
/organism="Arabidopsis thaliana"
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/ecotype="Col-0"
/db xref="taxon:3702"
/db xref="taxon:3702"
/db xref="taxon:3702"
/clone="sALK 112237.50.25.x"
/clone="FOR was performed on Arabidopsis thaliana lines"
/note="FOR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can
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ecotype="Col-0"
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/mol_type="genomic DNA"
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75.8%;
87.0%;
                                                   http://signal.salk.edu/tdna_protocols.html"
 Score 18.2; DB 8; Pred. No. 5.9e+02;
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ORIGIN

Query Match Best Local Similarity

片 S Matches 86 20; TTATGTAGACACGTCTTTCAAAG 24 TTATGTAGACAAGTATGTCAAAG 76 Conservative 0; Mismatches Indels 0, Gaps

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Search completed: February Job time: 2354.9 secs 9, 2005, 21:55:30 (otdsu) Andia again

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Result
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                           Score
  GenEmbl:*
1: gb ba:*
2: gb htg:*
3: gb in:*
4: gb ow:*
5: gb ow:*
6: gb pat:*
7: gb pat:*
9: gb pr:*
9: gb pr:*
11: gb sts:*
13: gb un:*
14: gb_v:*
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 February 9, 2005, 13:42:01; Search time 481.178 Seconds (without alignments) 2517.530 Million cell updates/sec
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Match
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Copyright (c) 1993 - 2005 Compugen Ltd.
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AX504324

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HUMMURIA02

1 G19985

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AR080193 Sequence
AR080192 Sequence
A38669 Sequence 1
M57450 Human multi
CQ806551 Sequence
AX457064 Sequence
AX598697 Sequence
                                                                AX504307 Sequence
AX504324 Sequence
AR080195 Sequence
AR080197 Sequence
AF345623 Homo sapi
AF345624 Homo sapi
AF36624 Homo sapi
AF36624 Homo sapi
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AR203322	AR091275	AC002457	AX707915	AX706985	AR363344	I08557	AR055785	HUMMDR1	AX504298	AX391099	AX336708	AX336420	AR380622	I49610	CQ861565	BD234195	AX587788	AX522070	CQ815440	CQ716151	HSMDR1A	AX825749	AX822109	AX795658	AX767353
AR203322 Sequence			_	_		Ò	AR055785 Sequence	M14758 Homo sapien	AX504298 Sequence			AX336420 Sequence		o	CO861565 Sequence				_		2			Sequenc	

ALIGNMENTS

RESULT 2 AX504324/c LOCUS DEFINITION ACCESSION VERSION VERSION VERSION KEYWORDS SOURCE ORGANISM	D Q	Query Match Best Local : Matches 2:	Source	JOURNAL	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 1 AX504307 LOCUS DEFINITION ACCESSION VERSION
AX504324 25 bp DNA linear PAT 27-SEP-2002 Sequence 27 from Patent WO0234291. AX504324 AX504324.1 GI:23386136 Homo sapiens (human)	1 GTGCTCAGCCCACGCCCCGGCGCTG 25	<pre>ch 100.0%; Score 25; DB 6; Length 25; l Similarity 100.0%; Pred. No. 41; 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	125 /organism="Homo sapiens" /mol_type="unassigned DNA" /mol_xref="taxon:9606"	multiple drug resistance Patent: WO 0234291-A 10 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) Location/Oualifiers	1 Colgan, S.P. Compositions and methods for treating hematologic malignancies and	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX504307 25 bp DNA linear PAT 27-SEP-2002 Sequence 10 from Patent WO0234291. AX504307 AX504307.1 GI:23386125

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DEFINITION
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                                                         1 (bases 1 to 351)
Stein, U. and Walther, W.
Vector for the expression of therapy-relevant
Patent: US 5968735-A 6 19-OCT-1999;
                                                                                                                      Unknown.
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                                                                                                                                                                                                                                                                                 1 GTGCTCAGCCCACGCCCCGGCGCTG 25
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Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 5 19-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5 from patent US
AR080196
                                                                                                            Unclassified.
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Patent: WO 0234291-A 27 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
Location/Qualifiers
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Mammalia; Eutheria;
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llarity 100.0%; 1
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          /mol_type="unassigned DNA"
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/mol_type="unassigned
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 370)

Alberta, E.O., Petersen, R.H., Hughes, K.W. and Lechner, B. Miscellaneous notes on Pleurotus
Persoonia 18, 55-69 (2002)

2 (bases 1 to 370)
   Submitted
                                                                                                                                             Homo sapiens
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               Wang, Y., Chen, G.K. and Sikic, B.I. Direct Submission
                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                         AF345624.1
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2. (bases 1 to 370)
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(06-FEB-2001) Oncology/Medicine, Stanford University
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/mol_type="mRNA"
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/chromosome="7"
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AR080195
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Sequence 3 from Patent WO03002760.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown
                               Distler, J. and Leu, E. Method for detecting cytosine methylation analysing single strands of amplificates patent: WO 03002760-A 3 09-JAN-2003;
                                                                                                     synthetic construct synthetic construct
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/chromosome="7"
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/note="vinblastine selected cell line"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMMDR1A02
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en,C.J., Clark,D., Ueda,K.,
                                                                                                                                                                                                                                                                                                       aft entry and computer-readable I.B.Roninson, 27-OCT-1989.
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larity 100.0%;
Conservative 0
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                         /map="7g21"
<1. .>976
                                                                                                                                                                                                /gene="PGY1"
/note="PGY1 m
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                    note="PGY1 mRNA and 69. .>976
                                                                                                                                                               gene="PGY1"
note="PGY1,
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                                                                                              note="PGY1,
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(MDR1) g
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Pred. No. 19;
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17;
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Ueda,K., Pastan,I. and Gottesman,M.M.
Isolation and sequence of the promoter region
multidrug-resistance (P-glycoprotein) gene
J. Biol. Chem. 262 (36), 17432-17436 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic organization of the human multidrug and origin of P-glycoproteins
J. Biol. Chem. 265 (1), 506-514 (1990)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 976)
                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Human multidrug resistant
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5' flank.
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                             Length 976;
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Length 976;

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Gaps

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PAT 31-AUG-2000

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                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human chromosome 7 STSs (1997)
Unpublished (1997)
Synonyms: PGY1
GDB: GDB:583426
GDB_DSEG: PGY1
Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      400
                                                                                                            This STS was developed from sequence determined by anot investigator. See GenBank record: M29423 For additional information about the NHGRI chromosome 7 mapping project, http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics 11:548-64 (1991) [MUID=92128937].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: egreen@nhgri.nih.gov
Primer A: AACGGAAGCCAGAACATTCC
Primer B: AGGCTTCCTGTGGCAAAGAG
STS size: 180
                                                                                                                                                                                                                                                                                 Buffer:
                                                                                                                                                                                                                                                                                                                                                                                        Protocol:
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National Human Genome Research
49 Convent Dr., MSC4431, Bldg.
Tel: 3014020201
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BWSS10 Eric D.
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Bouffard.G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunr
Bouffard.B.A., Mohr-Tidwell,R.M., Peluso,D.C., Fultor
Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fultor
Leckie,M.P. and Green,E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KCl:
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dNTPs:
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Total Vol:
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Annealing:
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                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
         /clone_lib="Eric D. Green"
l. .976
                                     map="7"
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each 200 uM
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sapiens STS genomic, sequence tagged
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49, Rm. 2A08, Bethesda, MD 20892
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                                                                                                                                            mapping project, see Also see Genomics
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HUMMDR1P/c
LOCUS
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AUTHORS
TITLE
JOURNAL
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AR080194/c
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AR080194
AR080194.1
                                                                                                                                                                                                                                                          MDR1 gene; P-glycoprotein; multidrug resistance protein Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                                                                                     Madden,M.J., Morrow,C.S., Nakagawa,M., Goldsmith,M.E., Fairchild,C.R. and Cowan,K.H.

Identification of 5' and 3' sequences involved in the regulation of transcription of the human mdrl gene in vivo

J. Biol. Chem. 268 (11), 8290-8297 (1993)
                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1327)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1318)
Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 3 19-OCT-1999;
Location/Qualifiers
                                                                           Original source text: Homo sapiens 4a) bone marrow DNA.
                                                                                                            8096520
                                                                                                                                                                                                                                                                                                                                                  Human multidrug resistant P glycoprotein
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                Location/Qualifiers
1. .1327
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/gene="PGY1"
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253. .432
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/mol_type="unassigned
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from patent US 5968735.
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100.0%; Pred. No. 16;
ative 0; Mismatches
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Pred. No. 17;
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PGY1)

PRI 09-JAN-1995 L) gene, 5'

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AUTHORS
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Sequence 2 from patent US 5968735.
AR080193
AR080193.1 GI:10006928
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                                 1 (bases 1 to 1688)
Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 2 19-OCT-1999;
Location/Qualifiers
                                                                                                               Unknown.
                                                                                                Unclassified.
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                                                                                                                                                                                                                                                                                                                     Similarity
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ilarity 100.0%;
Conservative 0
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863. .1171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="major transcription
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function="heat shock element"
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RESULT 14
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AR080192
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2117)
Stein, U. and Walther, W.
VECTOR FOR THE EXPRESSION OF THERAPY-RELEVANT GENES
Patent: WO 9411522-A 1 26-MAY-1994;
MAX DELBRUECK CT PUER MOLEKULA (DE)
Other publication DE 4238778 940519.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein, U. and Walther, W.
Vector for the expression of therapy-relevant genes
Patent: US 5968735-A 1 19-CCT-1999;
Location/Qualifiers
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			Gaps
			0;

Sequence Sequence

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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US-08-439-814-2
US-08-439-814-1
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US-09-927-561-2
US-08-927-561-2
US-09-925-40-1266
US-09-949-016-174342
US-09-949-016-16675
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Sequence 1179, Ap
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CURRENT APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: DE PCT/DE93/01086
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 91614-5015
REFERENCE/DOCKET NUMBER: 91614-5015
REJECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEPHONE: 202/638-5000
TELEPHONE: 202/638-6000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATION
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATION
PRIOR APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION NUMBER: WO PCT/DE93/01086
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: NIKAIDO, MARMELSTEIN, STREET: 655 Fifteenth Street, N. STREET: Street Lobby CITY: Washington
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US-08-487-811A-1
US-08-04-94-1
US-09-378-074-1
PCT-US93-07370-1
US-08-261-293-3
US-08-261-293-3
US-08-261-293-3
US-08-278-611-17
US-08-487-811A-17
US-09-378-074-17
PCT-US93-07370-17
US-08-056-51-3
US-09-38-074-17
PCT-US93-07370-17
US-08-056-51-3
US-08-056-651-3
US-08-056-651-3
US-08-056-651-3
US-08-056-651-3
US-08-487-811A-19
US-08-487-811A-19
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W., Suite 330
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
FILLING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: 202/638-5000
TELECAX: 202/638-4810
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APPLICANT: STEIN, Ulrike
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APPLICATION NUMBER: WO P
FILING DATE: 10-NOV-1993
(INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
                                                                         PRILING DATE: 12 NOV-1992
PRIOR APPLICATION DATA: MO PCT/DE93/01086
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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MEDIUM TYPE: Floppy disk
                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
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APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM STREET: 655 Fifteenth Street, N. W., Suite 330 STREET: Street Lobby
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Local Similarity 100.0%; Pred. No. 0.9
es 25; Conservative 0; Mismatches
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Pred. No. 0.93;
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                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: DE P 4
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                      FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PO
FILING DATE: 10-NOV-1993
                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, 1 PRIOR APPLICATION DATA: APPLICATION NUMBER: DE P4238778.7
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FILING DATE: 12-MAY-:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                             LENGTH:
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APPLICANT: WALTHER, WOLIGANG
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION
TITLE OF INVENTION: THERAPY-RELEVANT GENES
    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 202/638-5000
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KLESNER, Sharon N. REGISTRATION NUMBER: 36,335 REFERENCE/DOCKET NUMBER: P1
                                       STRANDEDNESS:
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                       COPOLOGY:
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STRANDEDNESS: singl
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                                                        H: 568 base pairs
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DNA (genomic)
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                                                          US-08-439-814-3
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Best Local
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PRIOR APPLICATION NUMBER: WO PC
APPLICATION NUMBER: WO PC
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
IENCRY. 1318 bags and the
Query Match
Best Local Similarity
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APPLICATION NUMBER: US/08/439,814
FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 4238778.7
PILING DATE: 12-MOY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/01086
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APPLICANT: STEIN, Ulrike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
ADDRESSES: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., Suite 330 G
STREET: Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, Sharon N.
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TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30B PRIOR APPLICATION DATA:
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TELEFAX: 202/638-4810
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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                                                                              MOLECULE TYPE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: KLESNER, Sharon N.
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
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                                                                                              TOPOLOGY:
                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Pred. No. 0.91;
   Score 25; DB 2;
Pred. No. 0.87;
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Patent No. 5968735
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GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
APPLICANT: WALTHER, WOLFGANG THE EXPRESSION
APPLICANT: OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFI
                                                                                   Query Match
                                                      Matches
                                                                    Best Local
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INFORMATION FOR SEQ ID NO:
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FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE PCT/DE93/010
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
PRIOR APPLICATION DATA:
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FILING DATE: 12-MAY-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: DE P
FILING DATE: 12-NOV-1992
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REFERENCE/DOCKET NUMBER: P1
                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                        TYPE: nucleic acid
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Pred. No. 0.86;
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Patent No. 5968735
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APPLICATION NUMBER: DE P 4
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION UMMER: DE PCT
APPLICATION UMMER: DE PCT
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
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APPLICATION NUMBER: US
FILING DATE: 12-MAY-19
CLASSIFICATION: 514
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APPLICANT: WAITHER, WOLIGANG
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ADDRESSEE: NIFICON, MARMELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth Street, N. W., Suite 330 G STREET: Street Lobby
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                                                                                                                                             Local
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: P1614-5015
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OPERATING SYSTEM:
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ER READABLE FORM:
LUM TYPE: Floppy disk
LUM TYPE: Floppy disk
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100.0%; Pred. No. 0.0
Live 0; Mismatches
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                                                                                                                                             0.85;
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US-09-023-655-1167/c
; Sequence 1167, Application US/09023655
; Patent No. 6607879
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                GENERAL INFORMATION:
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         CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                     APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                      TITLE OF INVENTION:
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NAME/KEY:
                                                          NUMBER OF SEQUENCES:
                                                                                                                               APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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APPLICANT: Lishko,
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STREET: 12526 High Bluff Drive, Suite 300
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                                                                                                  Susan G. Stuart
Jeffrey J. Seil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4646 base pairs
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                                                                                                                                Cocks, Benjamin G.
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425..4267
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                                                                      J. Seilhamer
COMPOSITION
EXPRESSION
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Waleryi K.
METHOD FOR DELIVERING BENEFICIAL
COMPOSITIONS TO HAIR FOLLICLES
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                                                                                                                                                                                                                                                                                                                           Score 25; DB 1;
Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                       FOR THE DETECTION OF BLOOD CELL GENE
                                                                                                                                                                                                                                                                                                                                      Length 4646;
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                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 9
US-08-583-276-18/c
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US-09-023-655-1167
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atent No. 5837536
GENERAL INFORMATION:
                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,27
FILING DATE: 05-JAN-1996
CIRCETECTION: 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-C
TELECOMMUNICATION INFORMATION:
TELECHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Word Perfect (CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: GENBA
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi & Stewart
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: McDonagh, Kevin APPLICANT: Nienhuis, Arthur APPLICANT: Tolstoshev, Paul
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APPLICATION NUMBER:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 ITLE OF INVENTION: ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                       STREET: 6 Becker Farm Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                      CITY: Roseland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 100.0%; Score 25; DB 4; Length 4646; socal Similarity 100.0%; Pred. No. 0.82;
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MULTIDRUG RESISTANCE GENES AND IMPROVED
SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kevin T.
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RESULT 11
5206352-3/c
;Patent No.
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5206352-3/c
;Patent No. 5206352
; AppLICANT: Roninson, Igor B.;Pastan Ira H.;Gottesman,
; Michael M.
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                                  5206352-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO:3:
                                                                 SEQ ID NO:3:
                                                                                                                                                                                                                               TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
                                                                                                                                                                                                                                                                   Michael M.
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Best Local Similarity
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Best Local (
Query Match
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APPLICATION NUMBER: 0:
FILING DATE: 22-MAY-1
INFORMATION FOR SEQ ID NO:
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
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DESCRIPTION: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
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LENGTH: 4669 bases
                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                APPLICANT: Roninson, Igor B.; Pastan Ira H.; Gottesman,
                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: singular
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 845,610 FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 892,575 FILING DATE: 01-AUG-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 4669
                                                                                                   APPLICATION NUMBER: 845,610
                                                                                                                 APPLICATION NUMBER: 892,575 FILING DATE: 01-AUG-1986
                                                   LENGTH: 4669
                                                                                FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocal Similarity
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     Score 25;
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   Length 4669;
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RESULT 13
US-09-316-167-1/c
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                                                                                                                                                                                                                        NAME/KEY:
; LOCATION:
US-08-752-447-1
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US-08-752-447-1/c
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
          Sequence 1, Application US/09316167
Patent No. 6365357
                                                                                                                                                              Matches
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/752,447
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: NO. 599408Bnan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELEPHONE: 312-913-0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applic
Patent No. 5994088
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Methods and Reagent TITLE OF INVENTION: Using Immunoligical
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                                                                                                                                                                                                                                                                                                                                                             EATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: McDoni
STREET: 300 Soutl
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
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                                                                                                  251 GCGCTCAGCCCACGCCCGGCGCTG 227
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                                                                                                                                                               Conservative
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425..4264
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1..424
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0 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                         CDNA
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mismatches
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for P-glycoprotein
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US-09-397-233-1/c;
Sequence 1, Application US/09397233;
Patent No. 6630327
; GENERAL INFORMATION:
                                                                                                                                                                                                                                         RESULT 14
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:

PRIOR APPLICATION UMBER: 08/752,44

APPLICATION NUMBER: 08/752,44

FILING DATE: 15-NOV-1996

ATTORNEY/AGENT INFORMATION:

NAME: No. 6365357man, Kevin E
REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 95,1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-213-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: SURVEY CHICAGO
CITY: Chicago
CITY: Illinois
TISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/316,167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4669 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-013-9808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COCATION:
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
                                                                                     TITLE OF INVENTION: Methods and Reagents for Preparing and Title OF Invention: Methods and Reagents Specific for P-glycoprotein
                                                                                                                                                 APPLICANT: Mechetner, Eugene
                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                          251
                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                       GTGCTCAGCCCACGCCCCGGCGCTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: McDonnell Boehnen Hulbert & Berghoff Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Roninson, Igor b
WENTION: Methods and Reagents for Preparing
VENTION: Using Immunoligcal Agents Specific
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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                                                                                                                                                                                                                                                                                                                                                                       93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kevin E
                                                                                                                                                                                                                                                                                                                                                     ; Score 23.4; D; Pred. No. 3.3; O; Mismatches
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for P-glycoprotein
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COUNTRY: USA
ZIP: 60606
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk

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Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08487141B Fatent No. 5683987
GENERAL INFORMATION:
APPLICANT: Smith, Larry J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPTULDED: PSTCATT PSTCATOR | 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Therapeuti
TITLE OF INVENTION: Targeting
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/487,141B FILING DATE: 07-JUN-1995 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION GATA:
SOCIETY OF THE STATE 
                                                                                                                                                                                                                                                                                                                                                                                                                                            STREE: Dann, Dorfman, Herrell and Skillman CITY: Philadelphia
STATE: PA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GCGCTCAGCCCACGCCCGGCGCTG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTGCTCAGCCCACGCCCCGGCGCTG 25
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24; Conservative
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
425..4264
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1..424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Therapeutic Oligonucleotides
Targeting the Human MDR1 and
US 08/379,180
                                                                                                                                                                                                                    #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MRP Genes
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                                                                                                                           ; ANTI-SENSE:
US-08-487-141B-2
                                                                                                                                                                                                   TELEPHONE: (215)563-4100
TELEPAX: (215)563-4044
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                           Query Match
Best Local Similarity
                                                              Matches 20;
                                                                                                                                                                                                                                                                                                              FILING DATE: 12-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
REFERENCE/DOCKET NUMBER: 6308
TELECOMMUNICATION INFORMATION:
                                                                                                                                           MOLECULE TYPE: DN
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                         TOPOLOGY:
                                1 GTGCTCAGCCCACGCCCCGG 20
GTGCTCAGCCCACGCCCCGG
                                                                Conservative
                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                      (215)563-4100
                                                                                                                                                                         DNA (genomic)
                                                            80.0%; Score 20; DB
100.0%; Pred. No. 82
ative 0; Mismatches
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 20
                                                                              DB 1; Length 20; 82;
                                                                 Indels
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Gaps

0

Search completed: February 9, 2005, 17:11:14 Job time : 79.592 secs

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Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM nucleic - nucleic search, using sw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
Published Applications NA:*

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2: /cgn2 6/prodate/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2 6/prodate/1/pubpna/US06 NEW PUB.seq:*

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22: /cgn2 6/prodate/1/pubpna/US10 NEW PUB.seq:*

22: /cgn2 6/prodate/1/pubpna/US10 NEW PUB.seq:*

22: /cgn2 6/prodate/1/pubpna/US10 NEW PUB.seq:*
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Gapop 10.0 , Gapext 1.0
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25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gtgctcagcccacgccccggcgctg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9, 2005, 13:42:02; Search time 266.667 Seconds (without alignments)
539.601 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No.
N N N N N N N N N N N N N N N N N N N	Score
1000.0	Query
44444453307 63307 466463307 466463	Query Match Length DB
18 9 18 13 14 11 11 17	DB
US-10-482-433A-3 US-09-805-020-31 18 US-10-473-126-37 US-09-805-020-30 13 US-10-072-621-2 14 US-10-097-340-1 15 US-09-968-007A-459 11 US-09-968-007A-747 17 US-10-641-643-1167 17 US-10-343-657-1	ID
Sequence 3, Appla Sequence 31, Appl Sequence 37, Appl Sequence 30, Appla Sequence 2, Appla Sequence 1, Appla Sequence 258, App Sequence 258, App Sequence 459, App Sequence 1167, App Sequence 1167, Appla Sequence 11, Appla	Description

RESULT 2 US-09-805-020-31/c

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18.2				18.2		18.2						٠				٠		18.2			18.4	18.4	18.4	18.6	18.6	18.6	18.6	18.6	18.6	9	19.2	23.4	N
72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8				74.4	74.4	74.4	•	•		76.8	٥.	•	٠
2738	2580	2383	23,25	2325	2128	1818	1763	1761	1610	1466	1370	1367	1250	750.	750	633	602	504	388	323	28049	4446	867	6073	6073	6073	706	604	556	2692	2692	4669	
13	17	18	18	9	17	18	17	17	14	14	14	15	17	17	13	18	18	16	14	18	18	17	18	16	15	13	18	18	9	片	ø	18	
US-10-052-586-575	US-10-092-900A-153	US-10-425-115-150283	-10-494-674-85	US-09-738-626-273	US-10-302-172-845	-10-437-963	-10-425-114	US-10-425-114-28838	-10-224-260	-10-224-260	-10-224-260	-10-241-313	-10-425-114-	-027-632-	-10-027-632-	-10	-10	-10-	-10 - 224	-10-	-10-	-10	-10-	-10	-10	US-10-024-623-16	US-10-767-701-5342	US-10-357-930-56850	US-09-864-761-13425	US-09-968-007A-755	US-09-880-107-3828	Ļ	
575,				Sequence 273, App	୍ଦ	æ	31892,	28838,	21,	19,	17,	3	14 14	164589,		Sequence 6, Appli		7696,	LINFOR	σ		1749	12083,	61,	66,	16,	e 534		13425,	e 755, A	282	- m	-

ALIGNMENTS

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                                                                                                                                                                                      OTHER INFORMATION: Amplification Product of MdRI-Fragment US-10-482-433A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-10-482-433A-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/10482433A
; Publication No. US20040265814A1
; CENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Method for the detection of cytosine methylation by comparative
; TITLE OF INVENTION: analysis of single strands of amplificates
                                                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 633
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                        Query Match 100.0%; Score 25; DB 1
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 82174
CURRENT APPLICATION NUMBER: US/10/482,433A
CURRENT FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: DE 10132212.7
PRIOR FILING DATE: 2001-06-27
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                    FEATURE:
422
                                              1 GTGCTCAGCCCACGCCCCGGCGCTG 25
GTGCTCAGCCCACGCCCCGGCGCTG 398
                                                                                                                                            DB 18; Length 633;
                                                                                                  Indels
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                                                                                                  Gaps
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Application US/09805020

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GENERAL INFORMATION:

APPLICANT: LEVINE, ZUTIT

TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES

FILE REFERENCE: 2786-0168P

CURRENT APPLICATION NUMBER: US/09/805,020

CURRENT FILING DATE: 2001-03-13

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 31

LENGTH: 2307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-473-126-37
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US-10-473-126-37/c
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                                                                                                                                                                                                     Sequence 30, Application US/09805020 Publication No. US20020086384A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 37
                                                                   SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 37, Application US/10473126
Publication No. US20040234973A1
GENERAL IMPORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
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Matches
                                                                              APPLICANT: LEVINE, ZULIE
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID MOS: 72
NUMBER OF SEQ ID MOS: 72
NUMBER OF SEQ ID MOS: 72
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Publication No.
              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (1)..(2307)
OTHER INFORMATION: any n = a,c,g,t any unknown or other
                                                 ENGTH: 4533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 2932
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                              1 GTGCTCAGCCCACGCCCCGGCGCTG 25
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                                                                                                                                                                                                                                                                                                                             GTGCTCAGCCCACGCCCCGGCGCTG 1015
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Pred. No. 0.16;
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Pred. No. 0.17;
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; LOCATION: (1)..(4533)
; OTHER INFORMATION: any n = a,c,g,t any unknown or
US-09-805-020-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-097-340-1/c
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US-10-072-621-2/c
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APPLICANT: Reiner, Peter B.

APPLICANT: Connop, Bruce P.

APPLICANT: Pollard, Michelle

TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION

TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ;

EILE REFERENCE: 100103.402

CURRENT APPLICATION NUMBER: US/10/072,621

CURRENT APPLICATION NUMBER: US/10/072,621

CURRENT FILING DATE: 2002-02-08

NUMBER OF SEQ. ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/10097340 Publication No. US20030087250A1
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Best Local (
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
                                                                              TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: MRI 030
                                                CURRENT APPLICATION NUMBER: US/10/097,340 CURRENT FILING DATE: 2002-03-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4643
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25; Conserv
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Steve G. KUVA...
Rachel E. MEYERS
Michael MORRISEY
Pater OLANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             John MONAHAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTCAGCCCACGCCCCGGCGCTG
                                                                                                                                                                                   Gordon B. MILLS
Robert C. BAST, Jr.
Karen LU
                                                                                                                                    Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                                                         Sebastian HOERSCH
Shubhangi KAMATKAR
                                                                                                                                                                      Rosemarie SCHMANDT
                                                                                                                                                                                                                                          Peter VEIBY
                                                                                                                                                                                                                                                                                                                                                                           Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Pred. No. 0.14;
0; Mismatches
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Pred. No.
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; SEQ ID NO 1
, LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-1
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                                                                                                   RESULT 8
US-09-968-007A-459/c
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PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR PILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-08-10
PRIOR PILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,502
PRIOR FILING DATE: 2001-09-19
PRIOR PILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
                                                                                                                                                                                                                                                                                                                                                        US-10-007-926A-258
                                    Sequence 459, Application US/09968007A Publication No. US20040115625A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 258
LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/254,090 PRIOR FILING DATE: 2000-12-08 NUMBER OF SEQ ID NOS: 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERTUCCI, FRANCOIS
APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                             FEATURE:
OTHER INFORMATION: atp-binding cassette, sub-family b
OTHER INFORMATION: (mdr/tap), member 1 (ABCB1) gene.
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                       Reinhard
                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 15; Length 4643; 100.0%; Pred. No. 0.14;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-459
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR PILING DATE: 2000-10-02
                                                                                                                                                                                         ; TYPE: DNA; ORGANISM: Homo sapiens US-09-968-007A-747
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
PRIOR PILING DATE: 2000-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 747, Applic Publication No. US20 GENERAL INFORMATION:
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Best Local :
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                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 747
                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1001
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 1001
                                                                                                                                                                                                                                                                   ENGTH: 4646
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251 GIGCICAGCCCACGCCCCGGCGCTG 227
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                                                GTGCTCAGCCCACGCCCCGGCGCTG 25
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                                                                                                   Conservative
                                                                                                                    100.0%;
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                                                                                                                       Score 25; DB 1
Pred. No. 0.14;
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US-10-343-657-1/c
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                                                                                                                                                                                                                  Sequence 1, Application US/10343657 Publication No. US20040086882A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                APPLICANT: Roninson, Igor B.
APPLICANT: Ruth, Adam
APPLICANT: Ruth, Adam
TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that Improve Its
TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs
FILE REFERENCE: 00,616-A
CURRENT APPLICATION NUMBER: US/10/343,657
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/222,313
PRIOR FILING DATE: 2000-08-01
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NUMBER OF
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APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNMBER: <Unknown>
FILING DATE: <Unknown>
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICAMAL.
Suban G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF
GENE EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            251 GTGCTCAGCCCACGCCCGGCGCTG 227
SEQ ID NOS: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE: g187468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (650) 855-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 4646 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; Dilarity 100.0%; Pred. No. 0.: Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 198
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-10-775-169-198
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US-10-775-169-198/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 198, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pred. No. 0.14;
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SEQ ID NO 1
LENGTH: 4646
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
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LOCATION: (425)..(4264)
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ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                           APPLICANT: Mechetner, Eugene
Roninson, Igor B
Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 GTGCTCAGCCCACGCCCGGCGCGCTG 227
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                                                                                                                                                     CITY: Chicago
STATE: Illinois
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                                                                                                                                   COUNTRY: USA
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for P-glycoprotein
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CLASSIFICATION: 435 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/680,516 FILING DATE: 07-Oct-2003

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NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3828
LENGTH: 2692
Type: Nor.
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                                     Query Match
Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-66-14
                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20020142981A1 X94563
                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: NOONAN, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/752,447 FILING DATE: 15-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: 3'UTR
LOCATION: 4265.4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: cDNA FEATURE:
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   1 GTGCTCAGCCCACGCCCCGGCGCT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 1..424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH: 4669 base pairs
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425..4264
                                     76.8%; Score 19.2; I
87.5%; Pred. No. 42;
ative 0; Mismatches
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                                                                            83
                                                                          9; Length 2692;
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HATFLICMAL: BUDGET, RELIGIBLE
HITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signal
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: Patentin version 3.0
SEQ ID NO 755
LENGTH: 2692
TYDE: DAMA
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ALIGNMENTS

RESULT 1 AAD39009/c

AAD39009 standard; DNA;

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AAD39009;

23-SEP-2002 (first entry)

Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; ds. Human mdr1 gene HIF-1 binding site DNA #2 25-OCT-2001; 02-MAY-2002. misc_binding Homo sapiens. Colgan SP; 26-OCT-2000; 2000US-0243542P WO200234291-A2 (BGHM) BRIGHAM & WOMENS HOSPITAL 2001WO-US049856 Location/Qualifiers /bound_moiety= "HIF-1" /*tag= a

ADB53945

MDR1 genc

binding molecules.

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1

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Best Local
Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
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XX ABV75271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (KING/) KING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A C.
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Pred. No.
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The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimerals are the promoter of the content of of th

The promoter chimera,

Example 1; Page 20;

48pp; English.

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                                           CC expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-cC specific promoter, intron or other unit transcription regulatory sequence of any length; and (c) a unit disease-cC of any length sensitive to genotoxic stress. The promoter chimera, and cC vector comprising the chimera are useful for in vivo or in vitro CC expression. The method is useful for the generation of improved CC expression constructs for in vitro and in vivo expression of the constructs for in vitro and in vivo expression of constructs for in vitro and in vivo expression of constructs for in vitro and in vivo expression of constructs and gene products. The HCMV IE-hNDR1 promoter CC chimeras of the present invention are more potent than either promoter ctanding alone. Sequences ABV75270-283 represent oligonucleotides used in CC che construction of promoter chimeras having hMDR1 disease specific DNA CC element and deletion of HCMV IE sequences not contributing to the CX activity of promoter chimera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoter; immediate
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early gene; gene therapy; ss.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                      100.0%;
                                                                                                                                                                                                                    11 C; 27 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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Pred. No. 4.1
0; Mismatches
                                                                                                          0
                                                                                                                                      Score 25;
Pred. No.
                                                                                                                Mismatches
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     27
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                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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                                                                                                                                                               Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 7
ABV75272/c
ID ABV752
XX
AC ABV752
XY
DT 07-MAR
XX
DE C3mut1
XX
KW Promot
KW Promot
KW immedi
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                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit diseasespecific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and expression. The method is useful for in vivo or in vitro expression constructs for in vitro and in vivo expression constructs for in vitro and in vivo expression of the present invention are more potent than either promoter chimeras of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the
         Promoter; immediate
                                                 C3mut1 construct creating sense oligonucleotide.
                                                                                 07-MAR-2003
                                                                                                                  ABV75272;
                                                                                                                                              ABV75272 standard; DNA; 56 BP
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 21; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-2002; 2002WO-US009882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3mut3 construct creating sense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABV75276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promoter; chimera; gene expression; viral; genotoxic; IE; hMDR1; immediate early gene; gene therapy; ss.
                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                     1 GTGCTCAGCCCACGCCCCGGCGCTG 25
                                                                                                                                                                                                                                                                                    Similarity 25; Conserv
                                                                                                                                                                                                                                                                                                                                               56
                                                                                                                                                                                                                        GTGCTCAGCCCACGCCCCGGCGCTG 27
   chimera; gene expression; viral; genotoxic; early gene; gene therapy; ss.
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                              BP; 10 A; 11 C; 27 G; 8 T; 0
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                 100.0%; Score 25;
100.0%; Pred. No.
tive 0; Mismatch
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                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                 4.1;
                                                                                                                                                                                                                                                                                                               DB 10; Length 56;
                                                                                                                                                                                                                                                                                                                                              U; 0 Other;
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                                                                                                                                                                                                                                                                                    Indels
                    IE; hMDR1;
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RESULT 8
ABV75283
ID ABV7
XX ABV7
XX ABV7
XX Prom
XX Prom
KW imme
XX Synt
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera and vector comprising the chimera are useful for in vivo or in vitro expression. The method is useful for the generation of improved expression constructs for in vitro and in vivo expression of the present invention are more potent than either promoter chimeras of the present invention are more potent than either promoter standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA element and deletion of HCMV IE sequences not contributing to the
             30-MAR-2001; 2001US-0280211P
                                         29-MAR-2002; 2002WO-US009882.
                                                                                                                                          Synthetic
                                                                                                                                                                                        Promoter;
                                                                                                                                                                                                                    C3 dimer and
                                                                                                                                                                                                                                                   07-MAR-2003
                                                                                                                                                                                                                                                                                  ABV75283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                           10-OCT-2002
                                                                                                          WO200279470-A1
                                                                                                                                                                    Promoter; chimera; gene expression; viral; genotoxic; IE; immediate early gene; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                 ABV75283 standard; DNA; 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 20; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-103274/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-MAR-2002; 2002WO-US009882.
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                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                            Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                               GTGCTCAGCCCACGCCCCGGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCTCAGCCCACGCCCCGGCGCTG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 BP; 10 A; 11 C; 27 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                    trimer constructs creating antisense oligonucleotide.
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB
Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                        hMDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RRESULT 9
RAW75277
ID ABV7
XX ABV7
XX ABV7
XX ABV7
XX Pron
CH Common CM immem
XX Pron
XX Synt

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transcription regulatory sequence of any length; and (b) a unit disease-
specific promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-
of any length sensitive to genotoxic stress. The promoter chimera, and
vector comprising the chimera are useful for in vivo or in vitro
expression. The method is useful for the generation of improved
expression constructs for in vitro and in vivo expression of
therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter
chimeras of the present invention are more potent than either promoter
standing alone. Sequences ABV75270-283 represent oligonucleotides used in
the construction of promoter chimeras having hMDR1 disease specific DNA
element and deletion of HCMV IE sequences not contributing to the
activity of promoter chimera
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                                              New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory
                                                                                                                                                                                                                                                                                                                                                                                             29-MAR-2002; 2002WO-US009882.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C3mut3 construct creating antisense oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-2003
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                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001US-0280211P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immediate
                                                                                                                                                                       WPI; 2003-103274/09
                                                                                                                                                                                                                                                                                 (KING/) KING A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dracreadeceacececedere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chimera; gere; early gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
llarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression;
ne; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 C;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             viral;
88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; Length 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genotoxic; IE; hMDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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The invention relates to a new promoter chimera for in vivo or in vitro cexpression that comprises: (a) a viral promoter, intron or other unit comparises: (a) a viral promoter, intron or other unit comparises: (b) a unit disease-cexpectific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and cexpression. The method is useful for in vivo or in vitro cexpression. The method is useful for the generation of improved cexpression constructs for in vitro and in vivo expression of the present jene products. The HCMV IE-hMDR1 promoter chimeras of the present invention are more potent than either promoter ce standing alone. Sequences ABV75270-283 represent oligonucleotides used in the construction of promoter chimeras having hMDR1 disease specific DNA celement and deletion of HCMV IE sequences not contributing to the contivity of promoter chimera
  Matches
                                      Query Match
                                                                                 Sequence 60 BP; 9 A; 28 C; 12 G; 11 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 21; 48pp; English.
                     Local
l Similarity
25; Conserv
Conservative
                     100.0%;
                                        100
  0; Mismatches
                       Score
Pred.
                       No.
                       4.1;
                                             DB 10; Length
                                                                                    U; 0 Other;
      0
        Indels
                                               60
      0
      Gaps
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07-MAR-2003
                                                                                                                                                                   C3mut1 construct creating antisense oligonucleotide
                                                                                                                                                                                                ABV75273 standard; DNA; 60
                                                                                                                                    WO200279470-A1
                                                                                                                                             Synthetic
                                                                                                                                                      Promoter; chimera; gene expression; immediate early gene; gene therapy;
                                                                                                                           10-OCT-2002
                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                GTGCTCAGCCCACGCCCCGGCGCTG 25
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                       30
                                                                                                                                                       88
                                                                                                                                                           viral; genotoxic;
                                                                                                                                                           IE; hMDR1;
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The invention relates to a new promoter chimera for in vivo or in vitro expression that comprises: (a) a viral promoter, intron or other unit transcription regulatory sequence of any length; and (b) a unit disease-specific promoter, intron or other unit transcription regulatory sequence of any length sensitive to genotoxic stress. The promoter chimera, and vector comprising the chimera are useful for in vivo or in vitro

expression. The method is useful for the generation of improved expression constructs for in vitro and in vivo expression of therapeutically-relevant gene products. The HCMV IE-hMDR1 promoter

New promoter chimera useful for in vivo or in vitro expression comprises viral promoter, intron or other transcription regulatory elements and disease-specific promoter, intron or other transcription regulatory

Page 21; 48pp;

English

WPI; 2003-103274/09.

30-MAR-2001; 2001US-0280211P 29-MAR-2002; 2002WO-US009882

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RESULT 11
ADR12342/
                Query Match
Best Local S
Matches 25
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                                                                                                                                                                                                                                                                     A method of identifying (MI) a compound that modulates untranslated region-dependent expression of a vascular endothelial growth factor (VEGF) gene comprises contacting a member of a library of compounds with a cell or cell-free translation mixture containing a reporter gene operably linked to an untranslated region (UTR) of the VEGF gene, and detecting expression of the reporter gene. A compound is identified as modulator if the level of expression of the reporter gene in the presence of the compound is altered as compared to that in the absence of the compound or in the presence of a control. Compounds identified by MI are useful for treating, preventing or ameliorating cancer or its symptoms, and/or for inhibiting angiogenesis. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimeras of the particular standing alone. If the construction element and delement and delement
                                                                                                                                                                             Sequence 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying modulators of untranslated region-dependent expression of a VEGF gene, useful for treating cancer, comprises contacting a compound with a cell or translation mixture containing a reporter gene linked to
                                                                                                                                                                                                                                                    therapeutic untranslated region used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; SEQ ID
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UTR-dependent expression; vascular endothelial growth factor;
untranslated region; cancer; angiogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PTCT-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention are more potent than either promoter one. Sequences ABV/5270-283 represent oligonucleotides used ction of promoter chimeras having hMDR1 disease specific DNA deletion of HCMV IE sequences not contributing to the promoter chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative (
                                                                                                                                                                             BP; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 9 A; 28 C; 12
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                                                                                                                                                                        A; 108 C; 111 G; 106 T;
        100.0%; Score 25; DI
100.0%; Pred. No. 3.0
Live 0; Mismatches
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Pred. No. 4.1
0; Mismatches
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                                              3.6;
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                                                                                        13;
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RESULT 13
ABX94595/c
ID ABX94s
XX
AC ABX94s
XX
AC 17-JUN
XX
DE Human
XX

ABX94595

ABX94595 standard;

DNA; 633

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Human MdrI 17-JUN-2003

DNA SEQ ID 3.

(first entry)

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RESULT 12
AAG62615/c
ID AAG62615 s
XX AAG62615;
XX I2-MAR-200
DT 17-JAN-199
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                                                                                                                   Matches
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                         This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, IL-2, IL-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New mammalian expression vector useful promoter and/or the enhancer of the md: cytostatic agents.
                                                                                                                                                                                                                            Sequence 568 BP; 142 A; 127 C; 143 G;
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                                                                                                                                           Similarity
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                                                     GTGCTCAGCCCACGCCCGGCGCTG 25
GTGCTCAGCCCACGCCCCGGCGCTG 390
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                                                                                                                Conservative
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                                                                                                                                     100.0%;
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                                                                                                                                        Score 25;
Pred. No.
                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful for gene therapy, - comprising the the mdr-1 gene which is susceptible to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention describes a novel method of determining cytosine CC methylation in a sample of genomic DNA which comprises treating the cample with hydrogen sulphite so that the cytosine is converted to uracil CC whilst 5-methylcytosine remains unchanged, amplifying sections of the DNA CC using at least 2 PCR primers and studying the base composition of both CC complementary amplified strands whereby methylation status is deduced CC from the difference in molecular weight of the two strands. The method is CC used to diagnose and/or prognose unwanted side effects of medication, CC cancer, central nervous system disorders, aggression symptoms or CC behavioural disorders, clinical, psychological and social consequence of CC brain damage, psychotic and personality disorders dementia and CC associated disorders, cardiovascular disease, malfunction, damage or CC disease of the gastrointestinal tract, breathing system, bone muscle, CC endocrine or metabolic system, injury, infection, abnormal development or Sexual malfunction. This sequence represents the human MdrI DNA fragment CC amplified by the PCR primers represented in ABX94593 & ABX94594 and is CC used to illustrate the method of the invention
DXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
ABZ83718/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining cytosine methylation in a genomic DNA sample by treating with hydrogen sulfite and analyzing the result, to diagnose associated conditions including cancer and brain disorders.
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WO2003016500-A2
                                                                                                                                                                                          Toxicologically relevant human nucleotide sequence #877
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                                                                                                                            Toxicologically relevant
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                                                                                                                            gene; toxicological response; gene;
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CC The present invention describes a method (M1) for determining a CC toxicological response to an agent, which comprises comparing the CC expression profile of one or more human toxic response genes to a CC reference gene expression profile indicative of toxicity, and so CC determining the presence of a toxic response to the agent. Also CC from the gene corresponding to the partial sequences given in ABZ82842 CC from the genes corresponding to the partial sequences given in ABZ82842 CC in ABZ84764, or their fragments of at least 20 nucleotides, or homologues (; and (2) determining if a gene putatively identified to be a toxic CC response gene plays a role on toxic response pathways by determining the CC expression profile of the gene after exposure of cells or a human subject to a known toxic pharmaceutical or industrial agent, comprising: (a) CC exposing cells to an agent or isolating the test gene expression profile (comparing the test possure to a known toxic pharmaceutical or industrial agent; and (c) comparing the test comparing the test profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or exposure to other known toxic compounds. The methods are useful for corresponded to the arrays comprising the human genes are useful for toxicological serential of compounds and chemicals or system level. The arrays comprising the human genes are useful for toxicological serential and chemicals
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AAQ62614/c
ID AAQ62
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                                                                      multiple drug resistance; mdr-1; mammalian cancer therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1024 BP; 287 A; 197 C; 260 G; 280 T; 0 U; 0 Other;
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                                                                                                                                                                                        25-MAR-2003
17-JAN-1995
                                                                                                                                                                                                                                                AAQ62614;
                                  Homo sapiens.
                                                                                                                                                    Human mdr-1 promoter fragment
                                                                                                                                                                                                                                                                                     AAQ62614 standard; DNA; 1318
                                                                                                              inducible promoter; cytostatic agent; adriamycin; vincristine;
                                                                                                                                                                                                                                                                                                                                                                                     251
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(first entry)
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Search completed: February 9, 2005, 16:05:54 Job time : 247.69 secs
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                                                                                                                                                                                                                                          This is a preferred fragment of the mdr-1 gene promoter, isolated from human DNA. The mdr-1 promoter and enhancer elements are inducible by cytostatic agents such as vincristine and adriamycin which are used in cancer therapy. Vectors comprising the promoter and enhancer sequences operably linked to heterologous genes coding for therapeutic agents are claimed. Using the vectors, the therapeutic agents (e.g. anti-oncogenes, interferon, II-2, II-6, etc.) can be expressed in cancer cells under the control of cytostatic agents. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                       Sequence 1318 BP; 430 A; 237 C; 277 G; 374 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mammalian expression vector useful for gene therapy, - comprising the promoter and/or the enhancer of the mdr-1 gene which is susceptible to cytostatic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 5; 7pp; German.
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                                                               1164 GTGCTCAGCCCACGCCCGGCGCTG 1140
                                                                                                1 GTGCTCAGCCCACGCCCCGGCGCTG 25
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                               Score
nucleic search, using sw
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1: gb
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Gapop 10.0 , Gapext 1.0
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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AW354719
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AV589422
CK846580
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BU376890
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CK646580 969088 MA
BM445737 IIL1B4.a
B1726148 1031083D0
BM431190 IDUcu11A00
BM431190 IDUcu11A00
BCB423537 596986 MA
BE212025 894027B01
BF216010 BP250003B
BX259366 BX259366
B0819612 1030079B0
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BU122038 603147071
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BU376890 603812819
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AL846843 CD874424 CN165319	CA692236 AL677976 AL960041	BG845541 BX107320 CO887857 BG904765	BG857646 BI720235 BQ808123 CK847926	BQ809798 BF045698 BM003827 BG855426	BF040164 BI527608 CO885514
AL846843 CD874424 CN165319		BG845541 BX107320 CO887857 BG904765		BQ809798 BF045698 BM003B27 BG855426	BF040164 BI527608 CO885514
AL846843 AZO3.102C 995732 MA	wlm96.pk0 AL677976 AL960041	BX107320 BovGen 16 Talr1134G	1024053B0 1031048E0 1030001F1 970621 MA	1030013D0 BP250023B 1031112H1 1024042F1	BP250023B 1024083A0 BovGen_13

ALIGNMENTS

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JOURNAL COMMENT
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BP218711/c
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Matches 2
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1 (bases 1 to 582)
Suzuki, Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Wizushima-Sugano,J., Nakai,K. and Sugano,S.
Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP218711 Sugano cDNA library, caudate nucleus Homo sapiens cDNA clone CNR05381, mRNA sequence.
BP348942 sugano cDNA library, brain SZR02494, mRNA sequence.
                                                                                                                                         1 GTGCTCAGCCCACGCCCCGGCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jap
Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                    Similarity
                                                                                                                   Grecreaeccaceccceecere
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                             /organism="Homo Bapiens"
/mol_type="nRNA"
/db_xref="taxon:9606"
/clone="CNRO5381"
/tissue_type="caudate nucleus"
/clone_lib="Sugano cDNA library, ca
                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                  100.0%; Score 25; DB 100.0%; Pred. No. 22;
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                                     mRNA
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                                                                                            18 1 (bases 1 to 280)
18 Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,
26 Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,
26 Alzawa, K., Akahira, S., Akimura, T., Arai, A., Arakawa, T.,
26 Alzawa, K., Hanagaki, T., Hiraoka, T., Hirozane, T.,
27 Hodoyama, Y., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kawai, J.,
28 Kojima, Y., Konno, H., Kusakabe, M., Matsuyama, T., Miyazaki, A.,
29 Nikamura, M., Nishi, K., Nomura, K., Namazki, R., Okazaki, Y.,
20 Okido, T., Owa, C., Sakai, K., Sasaki, D., Sato, K.,
20 Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
20 Shibata, K., Shibata, Y., Yasunishi, A., Yoshida, K., Yoshiki, A.,
20 Suzuki, H., Tagawa, A., Takahashi, F., Tanaka, T., Toya, T.,
21 Watahiki, A., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshiki, A.,
21 Muramatsu, M., and Hayashizaki, Y.
22 Muramatsu, M., and Hayashizaki
23 Laboratory for Genome Exploration Research Group, RIKEN Genomic
25 Sciences Center (GSC), Yokohama Institute
25 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
26 Tel: 81-45-503-9216
26 Fmail: Genome-research riken in IIDI.http.//genome-go-viten-in/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382
                         Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S.,
Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BB608269 RIKEN full-length enriched, 2 days pregnant adult female oviduct Mus musculus cDNA clone E230010F14 5', mRNA sequence.
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Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions
Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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/clone_lib="Sugano cDNA library, brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="SZR02494"
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  and thermoactivation of
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4022525 1
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Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg:1043, BARC-East, Beltsville, MD 20705, USA
                                                                                                                                                                                                                                                                                                                                              4022525 1GAL - Chicken Intestinal Lymphocyte
clone 1GAL_80L16 5', mRNA sequence.
CD737438
CD737438.1 GI:32288287
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                                                                                                         Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van Tassel,C. and Han,J.Y.
Chicken intestinal lymphocyte EST database as a resource for analysis of mucosal immune function
                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                       analysis of mucosal Unpublished (2003)
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Itoh, M., Kitsunai, T., Akiyama, Y., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y. and Hayashizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Site 1: Sall; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5]
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/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 652)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs (Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                    Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                      Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                               PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus (chicken)
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                                                                                                                                                                                     Simon.Hubbard@umist.ac.uk
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/cell type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="1GAL - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site_1
Sall; Site_2: Not!, Normalized library from chicken
infected with coccidia duodenum and middle gut."
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/sex="mixed"
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/db_xref="taxon:9031"
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mol_type="mRNA"
                                                                                               /organism="Gallus gallus"
/mol_type="mRNA"
                                    /strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST534814"
'lab_host="DH10B"
                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.8%;
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Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nRNA linear EST 28-NOV-2002 CDNA clone ChEST534a14 5', mRNA
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REFERENCE
AUTHORS
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BU122038/c
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KEYWORDS
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MEDLINE
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Best Local Similarity
Matches 22; Conserv
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BU122038
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Gallus gallus
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603147071F1 CSEQCHL17 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
Department of Biomolecular Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus.

1 (bases 1 to 738)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., I Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PO Box 88, Manchester, Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Department of Biomolecular Sciences 
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22335534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Simon.Hubbard@umist.ac.uk.
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/note="Organ: trunks; Vector: pBluescript II KS(+);
/note="Organ: trunks; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Ganome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01612360409
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/clone lib "CSEQCHL17"
/note="Organ: kidney + adrenal; Vector: pBluescript II
/RS(+); Site 1: EcoRI; Site 2: Not1; Modification of
RS(+); Site I: EcoRI; Site 2: Not1; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and EcoRI. Ligate in double stranded adaptor
                                                                                                                                                                                                                                                                                                                             /organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 15I"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                           clone="ChEST147n17"
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Pred. No. 1
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and Hubbard, S.
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BU287542/c
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                                         Best
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JOURNAL
MEDLINE
          Matches
                                                                        Query Match
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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      Similarity 88.
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1 (bases 1 to 816)

1 (bases 1 to 816)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Broard, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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BU287542
BU287542.1 GI:25736998
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603608037F1 CSEQCHN55 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                                                                                                       //dev stage="adult"
//lab host="DH10B"
//clone lib="CSEQCHN55"
//clone lib="CSEQCHN555"
//clone
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[5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattcttttttccggatccgggctgcacgc]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="ChEST593i10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"/
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                                     80.8%;
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Score 20.2; DB 5;
Pred. No. 1.4e+03;
0; Mismatches 3;
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Pred. No. 1.4e+03;
0; Mismatches 3
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                                                                 Length 816;
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RESULT 9
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VERSION
KEYWORDS
SOURCE
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BU376890/c
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Best Local S
Matches 22
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EST.
Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae;
BU845700 1000 bp mRNA linear ES' AGENCOURT_10414348 NIH_MGC_109 Homo sapiens cDNA clone
                                                                                                                                                                                                                              l Similarity
22; Conserv
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Phasianinae; Gallus.
1 (bases 1 to 929)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PO Box 88, Manchester, M60 1QD, Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Biomolecular Sciences University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      603812819F1 CSEQCHN74 Gallus
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                                                                                                                                                                                                                                                                                                                               /notes—Torgan: Kidney + adrenal; Vector: pBluescript II
KS(+); Site 1: EcoRI; Site 2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="ChEST802e5"
|sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="Compton Line 15I"
/db_xref="taxon:9031"
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Pred. No. 1.3e+03;
0; Mismatches 3;
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gallus cDNA clone ChEST802e5 5', mRNA
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BU845700
BU845700.1 GI:24030141
                                                                                                                                                                                                                                                                            AGENCOURT 7594073 NIH MGC 70 5', mRNA Bequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
plate: LLCM2782 row: j column: 17
High quality sequence start: 14
High quality sequence stop: 443.
Location/Qualifiers
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Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/
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                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                    Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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Unpublished (1999)
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                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                BQ219968.1 GI:20401357
cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                (bases 1 to 1017)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="teratocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone lib="NIH MGC 109"
/clone lib="NIH MGC 109"
/note="Torgan: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2: /note="Corgan: ovary; Vector: pOTB7; Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6579377"
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Pred. No. 1.3e+03;
0; Mismatches 3;
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sapiens
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IMAGE:6021580
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM13227 row: i column: 05
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                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 4 Row: f Column: 17
This clone has the following problem: retained intron.
                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg, R
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute, 31 Center Drive, Room 11A03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGCTCTGCCCCCCCCCCGGCGCTG 108
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/clone="IMAGE:6021580"
/tissue_type="epithelloid carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC_70"
/clone_Tib="NIH MGC_70"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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/tissue_type="Cervix, carcinoma"
/clone_lib="NIH_MGC_12"
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                                                         clone="IMAGE:3456552"
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Pred. No. 1.3e+03;
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Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                FORWARD: AGGARACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 9 row: M column: 16
Seq primer: TAATACGACTCACTATAGGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eut
Bovinae; Bos.
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36851 MARC 4BOV Bos taurus cI
AW354719
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH108"
/lab_host="DH108"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                                                                                                                                                                                 organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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/note="Vector: pC
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87.5%;
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Pred. No. 3.7e
0; Mismatches
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                                                                                                                                              Length 319;
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                                                                                                                                                                                                                                         AV589422
AV589422
3', mRNA
AV589422
                            Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimoto,Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                        AV589422.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                bovine ESTs
                                                                                                                                                                                      Bos taurus (cow)
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Shirakawa Institute of Animal Genetics
Odakura, Nishiso, Nishi-shirakawa, Fuku
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV663420 4
AV663420 Bos taurus brain
3', mRNA sequence.
AV663420 .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single pass sequencing.
This clone was obtained from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 29
21570554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: kazusugi@cocoa.ocn.ne.jp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV663420.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      povine ESTS
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                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTCAGCCCACGCCCCGGCGCTG 25
                                                                                                 (bases 1 to 452)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 401)
                                                                                                                                                                                                                                                           mRNA sequence.
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Acids Res.
                                                                                                                                                                                                                                                                         Bos taurus brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clome_lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 sīte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9913"
/clone="E1BR036E05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="brain"
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/mol_type="mRNA"
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Pred. No. 3.6e+03;
0; Mismatches 3
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CDNA clone E1BR006D03
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ne E1BR036E05
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CK846580/c
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
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11713328
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heston, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.

Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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This clone was obtained from a polyA-deleted cDNA library.
Location/Qualifiers
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                                                                                                                                                                   Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and strimmed with the aid of the trim_alt option. Vector identified with the sid of the trim_alt option.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CK844580 485 bp mRNA linear
969088 MARC 4BOV Bos taurus cDNA 3', mRNA sequence.
CK846580
CK846580.1 GI:45207234
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                                                                                  cross match v0.990329.
Plate: 74 row: H column: 8
Seq primer: GTAATACGACTCACTATAGGG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="Bos taurus brain fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly A
was deleted from a Not1 site"
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/organism="Bos taurus"
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87.5%; Pred. No. 3.5e+03;
tive 0; Mismatches 3; Indels
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Search completed: February
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/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled tissue from day 20 and day 40 embryos."
                                                                                                                                          76.8%; Score 19.2; DB 7;
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nucleic search, using sw model
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1: gb_ba:*
2: gb_htg:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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JOURNAL FEATURES SOURCE	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 1 AX504308 LOCUS DEFINITION ACCESSION VERSION		4 4 5	C 42 1	44		37 38	c 35	ωυ 142-0	3 2	3 5 1 0		27 28				22 1	ــر مــر	
Patent: WO 0234291-A 11 02-MAX-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) Location/Qualifiers 125 CCe 125 /mol_type="unassigned DNA" /mol_type="unassigned DNA"	Colgan, S.P. Compositions and methods multiple drug resistance	. Homo sapiens (human) M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX504308 25 bp DNA linear PAT 27-SEP-2002 N Sequence 11 from Patent WO0234291. AX504308 AX504308.1 GI:23386126	ALIGNMENTS	.2 76.8 300350 .2 76.8 346542.	76.8 260600 2 AC115307 AC115307 Rattus	.2 76.8 240053 2 AC113002 AC113002	.2 76.8 221430 2	6.8 207584 2 AC103892 AC103892 AC123206 Rattus 6.8 216892 2 AC123206 AC123206 Rattus	.2 76.8 1984/8 2 ACL1/692 ACC91288 ACC9	.2 76.8 194313 5 BX323807 BX323807 Zeb	.2 76.8 181004	6.8 179880 4 AC150482 AC150482 Bos ti	.2 76.8 151750 9 AC003666	.2 76.8 130460 5 ACU98806 ACU51162 Bos to ACU51162 Bos to ACU51162 ACU51162 Bos to ACU5164 Bos	9.2 76.8 129814 9 AC116614	9.2 76.8 96335 IU ACU/329/ 9.2 76.8 121813 2 AC147587	9.2 76.8 67699 8 AE016815_8 Continuati	9.2 76.8 59032 10 BX005046 BX005046 Mouse	9.8 79.2 349926 1 BX571660 E	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0

Query Match Best Local Similarity 100.0%; Score 25; DB 6; Length 25; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps Qy 1 CCAGCATCTCCACGAAGGCAGAGTT 25	ORIGIN	/db_xref="taxon:9606"		
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1 CCAGCATCTCCACGAAGGCACAGTT 25 /c AX504325 N AX504325 N AX504325 N AX504325 Homo sapiens (human)	δ	1 CCAGCATCTCCACGAAGGCAGAGTT 25		
/c AX504325 ON Sequence 28 from Patent WO0234291. N AX504325 AX504325.1 GI:23386137 Homo sapiens (human)	DЪ	1 CCAGCATCTCCACGAAGGCAGAGTT 25		
AX504325 25 bp DNA linear Sequence 28 from Patent WO0234291. AX504325 AX504325.1 GI:23386137 Homo sapiens (human)	RESULT 2 AX504325/c			
z	LOCUS	DNA linear	PAT	27-S
	ACCESSION	Sequence 28 from Patent WO0234291. AX504325		
1	VERSION	AX504325.1 GI:23386137		
	SOURCE	Homo sapiens (human)		

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Isolation and sequence of the promoter region
multidrug-resistance (P-glycoprotein) gene
J. Biol. Chem. 262 (36), 17432-17436 (1987)
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J. Biol. Chem. 265 (1), 506-514 (1990)
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Patent: WO 0234291-A 28 02-MAY-2002;
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/note="PGY1 mRNA (
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PUBMED REFERENCE

AUTHORS

JOURNAL MEDLINE TITLE

FEATURES

This STS was developed from sequence determined by anolinvestigator. See GenBank record: M29423 For additional information about the NHGRI chromosome 7 mapping project, http://www.nhgri.nih.gov/DIR/GTB/CHR7. Also see Genomics

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STS.
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Unpublished (1997)
Synonyms: PGY1
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1 (bases 1 to 976)

Bouffard,G.G., Iyer,L.M., Idol,J.R., Braden,V.V., Cunningham,A.F., Weintraub,L.A., Mohr-Tidwell,R.M., Peluso,D.C., Fulton,R.S., Leckie,M.P. and Green,E.D.
A collection of 1814 human chromosome 7-specific STSs
Genome Res. 7 (1), 59-64 (1997)
                                                                                                                                Protocol:
                                                                                                                                                                                                                                  Email: egreen@nhgri.nih.gov
Primer A: AACGGAAGCCAGAACATTCC
Primer B: AGGCTTCCTGTGGCAAAGAG
                                                                                                                                                                                                                                                                    National Human Genome Research
49 Convent Dr., MSC4431, Bldg.
Tel: 3014020201
Fax: 3014024735
                                                                                                                                                                                                                                                                                                               GDB_DSEG: PGY1
Contact: Eric D. Green
Genome Technology Branch
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Annealing:
Polymerization:
PCR Cycles:
  MgCl2:
KCl:
Tris-HCl:
pH:
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Total Vol:
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Location/Qualifiers
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25; Conserv
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Sequence 136 from Patent
AX597862
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                       Homo sapiens (human)
                                                                               CQ806551
Sequence 1 from Patent 1
CQ806551
CQ806551.1 GI:47111933
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             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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complement(413.
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253. .272
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253. .432
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1. .976
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Catarrhini; Hominidae;
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25; Conserv
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AX457064
AX457064.1 GI:21715846
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Patent: WO 2004035803-A 1 29-APR-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marx,A.
Berlin,K., Braun,A., Distler,J., Guetig,D., Howe,A., Mueller,J., Olek,A., Piepenbrock,C., Adorjan,P., Grabs,G., Lesche,R., Leu,E., Lewin,A., Lipscher,E., Maier,S., Model,F., Mueller,V., Otto,T., Pelet,C. and Ziebarth,H.

Methods and nucleic acids for the analysis of hematopoietic cell
                                                                                                                                                                                Sequence 37
AX598697
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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AX795658/c
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Sequence 1 from Patent WO03052135.
AX795658
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Sequence 1 from Patent W003044226.
AX767353
                                                    Method and nucleic acids for the analysis of a lung cell proliferative disorder Patent: WO 03052135-A 1 26-JUN-2003;
                                                                                                                                                                   Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                        Epigenomics AG (DE)
                                                                                             and Nimmrich,
                                                                                                            Burger, M., Field, J.K., Genc, B., Liloglou, T., Lipscher, E.,
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                  Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Method and nucleic acids for the analysis
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/organism="Homo sapiens"
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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/mol_type="unassigned DNJ
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100.0%; Pred. No. 0.59;
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Pred. No. 0.59;
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 1 from Patent WO03072821.
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Sequence 1 from Patent
AX822109
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Method and nucleic acids for the analysis
proliferative disorder
Patent: EP 1340818-A 1 03-SEP-2003;
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Patent: WO 03072821-A 1 04-SEP-2003;
                                                                                                                                                          Adorjan, P., Burger, M., Rujan, T. and Schmitt, A.
                                                                                                         Epigenomics AG (DE)
                                                                                                                                                  Method and nucleic acids for the analysis of a colon cell
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.5
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Submitted (04-APR-1991) N. Kioka, Laboratory of Biochemistry, of Agricultural Chemistry, Kyoto University, Kitashirakawa Oiwake-cho, Sakyo-ku Kyoto 606, JAPAN See Jpn. J. Cancer Res. 80:1127-1132(1989) for overlapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 2932)
Kioka,N., Yamano,Y., Komano,T. and Ueda,K.
Kioka,N., Yamano,Y., Komano,T. and Ueda,K.
Heat-shock responsive elements in the induction of the multidrug resistance gene (MDR1)
FEBS_Lett. 301 (1), 37-40 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-glycoprotein gene (MDR1) cDNA from human adrenal: normal P-glycoprotein carries Gly185 with an altered pattern of multidrug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2932)
Kioka,N., Tsubota,J., Kakehi,Y., Komano,T., Gottesman,M.M.,
Pastan,I. and Ueda,K.
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Heinrich,G. and Kerb,R.
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Epidauros Biotechnologie AG (DE)
Location/Qualifiers Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. DNA linear based on CYP3A5 PAT 04-APR-2003

Heinrich,G. and Kerb,R. Methods for treatment of cancer using Patent: WO 03013536-A 683 20-FEB-2003; Epidauros Biotechnologie AG (DE) Location/Qualifiers Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Score 25; DB 6; Length 177380; Pred. No. 0.53; DNA irinotecan <u>,</u> linear based on UGT1A1 PAT Euteleostomi; Homo 0 04-APR-2003 Gaps 0

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US-09-949-016-17362 US-09-902-540-5803 US-09-902-540-1273 US-09-489-039A-294 US-09-489-039A-295 US-09-489-039A-295 US-09-489-039A-419 US-09-489-039A-419 US-09-489-039A-419 US-09-489-039A-419 US-09-16-434-1477 US-09-16-434-1477 US-08-365-486A-18 US-09-949-016-1116 US-09-949-016-3696 US-09-949-016-3696 US-09-949-016-3696 US-09-949-016-3696 US-09-949-016-3696 US-09-949-016-3696 US-08-365-486A-20 US-09-123-708-3	w	N	4.	4.	w	N	4.	4	4	4.	4	4	ω	4	4	4	4	
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ALIGNMENTS

US-09-949-016-189127

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Sequence 189128, Application US/09949016

| Sequence 189128, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION: APPLICANT: VENTER, J. Craig et al.
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION APPLICATION NUMBER: US/09/949,016
| CURRENT APPLICATION NUMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR APPLICATION NUMBER: 60/237,768
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-30
| PRIOR FILING DATE: 2000-10-03
| PRIOR APPLICATION NUMBER: 60/231,498
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PRIOR OF THE CONTROL NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
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; ORGANISM: Human
US-09-949-016-189127
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
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90.9%;
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Pred. No. 6
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; SEQ ID NO 13079
LENGTH: 2028
; TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13079
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US-09-949-016-17153/c
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US-09-949-016-17153
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SEQ ID NO 17153
LENGTH: 76401
TYPE: DNA
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 189128
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Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
FILE REFERENCE: CLO01307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                  PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                            TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                       APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                   NUMBER OF SEQ ID NOS:
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TYPE: DNA
ORGANISM: Human
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90.9%;
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90.9%;
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Pred. No. 1.3e+02;
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Pred. No. 6
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US-09-252-991A-12708
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GENERAL INFORMATION:
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SEQ ID NO 12708
LENGTH: 3525
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GENERAL INFORMATION:
                                                                                                                                                                                              SEQ ID NO 13251
LENGTH: 3906
                                                                      Matches
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Best Local
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Best Local Similarity
Matches 21; Conserv
                                                                                       Query Match
Best Local (
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 199-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
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                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
                                                                                                                                                             TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
 2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1998 CCAGCTTGTGCACGAAGGAAGAGTT 2022
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                                  1 CCAGCATCTCCACGAAGGCAGAGTT 25
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                                                                                       Similarity
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Similarity 84.0%;
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                                                                      Conservative
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                                                                Score 18.6; DB 4
Pred. No. 1e+02;
0; Mismatches
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Pred. No. 95;
0; Mismatches
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2194
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                                                                                                      Length 3906;
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FABSUSEQ for Windows Version 4.0
SEQ ID NO 164913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEWART, Alexand APPLICANT: LARKIN, Sarah B. TITLE OF INVENTION: DTEF-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20, Application US/08615170
>. 5776776
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AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAR, Janet H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORDAHL, Charles
AZAKIE, Anthony
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alexandre F.R.
                                                                                                                                                                                                                         US/08/615,170
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Pred. No. 1.2e+02
0; Mismatches
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; MOLECULE TYPE:
US-08-615-170-20
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01526
FILING DATE: 06-FEB-1995
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/191,493
FILING DATE: 04-FEB-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
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              TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
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TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LARKIN, Sarah B.
TITLE OF INVENTION: DTEF-1 ISOFORMS AND USES THEREOF NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/615,170
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                             TELEPHONE: (415)
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STRANDEDNESS:
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AZAKIE, Anthony
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                                                                                                       (415) 326-2400
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87.0%;
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Pred. No. 1.4e+02;
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RESULT 11
US-08-387-942C-1
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4640
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Applic Patent No. 5939289
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Best Local Similarity 87.0%;
Matches 20; Conservative
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Patent No. 681201
Patent INFORMATION:
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TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILLING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ERTESV
                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                        ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, ST
STREET: P.O.BOX 747
                                                                                                                                                                                                                                                                                         APPLICANT: LARSEN, BJORN
TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
TITLE OF INVENTION: ENCODING MANNURONAN C-5-EPIMERASE
                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                       STREET: P.O.BOX 74
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Local Similarity 87.0%;
APPLICATION NUMBER:
                                                                                                                                                     COUNTRY:
                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
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                                                                                                                                                                                                                                    STEWART, KOLASCH & BIRCH, LLI
US/08/387,942C
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    Mismatches

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Pred. No. 1.4e+02;
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Pred. No. 1.4e+02;
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; Sequence 16382, Application US/09949016
; Patent No. 6812339
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                                  Query Match
Best Local Similarity 87.0
Conservative
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Best Local Similarity 87...
20; Conservative
                                                                                                                                                SEQ ID NO 16382
LENGTH: 36103
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J.
                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                            APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIENS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12588 base pairs
                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 28,977
REFERENCE/OOCKET NUMBER: 18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
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NAME: MURPHY JR, GERALD M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 12588 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8771 CCAGCAACTCCTCGAAGGCAGCG 8793
1 CCAGCATCTCCACGAAGGCAGAG 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAGCATCTCCACGAAGGCAGAG 23
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6702..9695
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290..1951
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2227..6438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single
                                                                                                                                                                                                            2000-09-08
                                                          72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.8%;
87.0%;
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Pred. No. 1.8e
0; Mismatches
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                                              0; Mismatches
                                                            Score 18.2; DB 4;
Pred. No. 2.1e+02;
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                                                                        Length 36103;
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                                              Indels
                                              0,
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                                              Gaps
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16613 CCAGCACCTCCACGAAAGCTGAG 16591

US-09-949-016-15083

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GENERAL INFORMATION: Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

FULRENT TEILING DATB: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASKEEQ for Windows Version 4.0

SEQ ID NO 15084

LENGTH: 50850
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                                                                            ; FEATURE:
, NAME/KEY: misc feature
; LOCATION: (1)...(50850)
; OTHER INFORMATION: n = A,T,C
US-09-949-016-15084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-949-016-15084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 50850

TYPE: DNA
ORGANISM: Human
PEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(50850)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15084, Application US/09949016 Patent No. 6812339
Query Match 72.8%;
Best Local Similarity 87.0%;
Matches 20; Conservative
                                                                                                                                                                          ORGANISM: Human
                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 CAGACTCTCCACAAAGGCAGAGT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CAGCATCTCCACGAAGGCAGAGT 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.8%;
                                                                                                  or G
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Pred. No. 2.2e+02;
0; Mismatches 3;
    Score 18.2; DB 4;
Pred. No. 2.2e+02;
0; Mismatches 3;
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                                        Length 50850;
        Indels
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      Gaps
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B--- 5
                                                                                                                                                              ; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(50850)

; OTHER INFORWATION: n =

US-09-949-016-15085
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FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSTSEQ for Windows Version 4.0
SEQ ID NO 15085
LENGTH: 50850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15085, Application US/09949016 Patent No. 6812339
                                                                    Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 CAGACTCTCCACAAAGGCAGAGT 534
  512 CAGACTCTCCACAAAGGCAGAGT 534
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                                        2 CAGCATCTCCACGAAGGCAGAGT 24
                                                                               Conservative
                                                                                                    72.8%;
87.0%;
                                                                                                                                                                                     A, T, C or
                                                                                 0
                                                                                                      Score 18.2; DB 4;
Pred. No. 2.2e+02;
                                                                                   Mismatches
                                                                                                                           DB 4;
                                                                                                                         Length 50850;
                                                                                     0
                                                                                     Gaps
                                                                                       0
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Sequence 15083, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

Search completed: February 9, 2005, 17:11:16
Job time : 80.592 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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	7:	/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
	8	/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
	9:	/cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
	10:	/cgn2 6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
	11:	
	12:	/cgn2 ⁻⁶ /ptodata/1/pubpna/US09_NEW_PUB.seq:*
	13:	/cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
	14:	/cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
	15:	
	16:	/cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
	17:	/cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
	18:	
	19:	
	20:	/cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
	21:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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3058	2963	2963	2914	2797	60	619	561	2932	1021	Length	
9 17	17	17	17	17	10	18	18	18	17	DB	
US-10-336-603A-11 US-09-964-824A-234	US-10-440-464-125	US-10-444-575-5	US-10-336-603A-9	US-10-336-603A-7	US-09-908-975-9939	US-10-425-115-59217	US-10-767-701-25185	US-10-473-126-37	US-10-321-039-24	ID	SUMMARIES
Sequence 11, App Sequence 234, App	Sequence 125, App	Sequence 5, Appli	Sequence 9, Appli	Sequence 7, Appli	Sequence 9939, Ap	Sequence 59217, A	Sequence 25185, A	Sequence 37, Appl	Sequence 24, Appl	Description	

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17.8	17.8	17.8	17.8	•	17.8		17.8	•		18	18	18	18	18	18	18	18		•	18.2	•	•	•	٠		18.2	•	18.2	•	•	•	•	18.6
	71.2	•	•		•	•		•					72.0	72.0	72.0	72.0	72.0	72.8	72:8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8	72.8		74.4	74.4	74.4
1146	1003	1003	1003	1003	1003	. 1003	575	575	358	493999	6638	6519	2524	2524	201	201	201	57013	2713	2345	2196	2083	1717	1643	1422	1346	945	945	494	494	684187	8	3058
-	17	17	17	13	13	13	11	11	17	18	18	18	17	17	18	18	18	13	9	15	13	17	9	9	18	9	17	13	17	13	18	17	9
N2-10-362-453-45215	10-027-632-15319	0-027-632-	-10-027-632-12097	-10-027-632-120	-027-632-12097	US-10-027-632-120970	-09-876-143-	9-876-143-2	0-062-674-	-10-719-993-	US-10-719-993-108	-719-9	-10-152-319F	1-115	US-10-719-993-13683	Ÿ	3-204	179	US-09-805-020-27	US-10-101-510-504	US-10-087-192-1799	9-563-289	09-805-020-2	US-09-805-020-26	÷	-02	-10-027-	10-027-632-3	-10-027-632-	-10-027-632-23010	-10-367-	-10-336-603A-	US-09-880-107-1654
seducire sorts, o	e 1209/2,	0	Ф	Œ	æ	Œ	e 314,	e 226,	e 773,	6787,	108,	Sequence 109, App	2092,	Sequence 115, App	13683	209	2047,	17	7	ጥ	17	e 289, 7	24, A	26,	ø	25, App1	Sequence 30739, A	e 30739,	equence 230104,	2301		5, Appl	54, Ap

ALIGNMENTS

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APPLICANT: Lukowiak, Andrew
APPLICANT: Lukowiak, Andrew
APPLICANT: Jarvis, Nancy
CURRENT APPLICATION: Amplification Methods and Compositions
FILE REFERENCE: FORS-06960
CURRENT APPLICATION NUMBER: US/10/321,039
CURRENT APPLICATION NUMBER: 09/998,157
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/329,113
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR APPLICATION NUMBER: 60/360,489
PRIOR PILING DATE: 2001-10-19
NUMBER OF SEG ID NOS: 759
SOFTWARE: PatentIn version 3.2
SEG ID NO 24
LENGTH: 10/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-10-321-039-24
J Sequence 24, Application US/10321039
Publication No. US20040014067A1
GENERAL INFORMATION:
                                                                                                                              US-10-321-039-24
Query Match 100.0%; Score 25; DB 17; Length 1021; Best Local Similarity 100.0%; Pred. No. 0.076; Matches 25; Conservative 0; Mismatches 0; Indels 0.
                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (561)..(561)
OTHER INFORMATION: n can be t or c.
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1021
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0;

Gaps

0,

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US-10-767-701-25185

/ Sequence 25185, Application US/10767701

/ Publication No. US20040172684A1

/ GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

/ APPLICANT: Cao, Yongwei

/ TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules and Other Molecules of INVENTION: Plants and Uses Thereof For Plant Ing

/ FILE REFERENCE: 38-21(5353) B

/ CURRENT APPLICATION NUMBER: US/10/767,701

/ CURRENT PILING DATE: 2004-01-29

/ NUMBER OF SEG ID NOS: 63128

/ SEQ ID NO 25185

/ ELENCTH: 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-473-126-37/c
US-10-473-126-37/c
; Sequence 37, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cel:
                                                                                                                                       RESULT 4
US-10-425-115-59217
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                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: 30948191 US-10-767-701-25185
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                                                                                   Sequence 59217, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         Best Local
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 37
                                               APPLICANT: La Rosa, Thomas APPLICANT: Kovalic, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 2932
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Zhou, rime
                                                                                                                                                                                                                                                   CAGCATCTCCACGAAGGCAGAGTT 25
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                                         Kovalic, David K.
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 18 ilarity 100.0%; Pred. No. 0.075; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                       76.8%;
87.5%;
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                         Score 19.2;
Pred. No. 39;
                                                                                                                                                                                                                                                                                        Mismatches
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US-10-336-603A-7/c
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                                                                                                                                                             Sequence 7, Application US/10336603A Publication No. US20040072997A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 9939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9939, Application US/09908975
Publication No. US20030165843A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(5322)B FILE REFERENCE: 38-21(5322)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 59217 LENGTH: 619
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Best Local Similarity
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Best Local Similarity
                                                          APPLICANT: Alsobrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILLING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Bli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE 1
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/287,724 PRIOR FILING DATE: 2001-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Zea mays
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87.5%;
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Pred. No. 76;
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Pred. No. 39,
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LENGTH: 2797

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (130)..(2658)
US-10-336-603A-7
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TYPE: DNA
CORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (130)..(2775)
US-10-336-603A-9
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SOFTWARE: CuraSeqList version
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
APPLICANT: Alsobrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 169
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 9
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Best Local S
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          APPLICANT: Kuchel, George A
APPLICANT: Zhu, Qing
TITLE OF INVENTION: Compositions and Methods Relating to Detrusor Estrogen-Regulated
TITLE OF INVENTION: Protein (DERP)
FILE REFERENCE: UCT-0035
CURRENT APPLICATION NUMBER: US/10/444,575
CURRENT FILING DATE: 2003-05-22
PRIOR APPLICATION NUMBER: US 60/382,830
PRIOR APPLICATION NUMBER: US 60/382,830
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
SEQ ID NO 5
                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                 APPLICANT: University of Connecticut Health Center APPLICANT: Kuchel, George A
LENGTH: 2963
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1 Similarity 84.0%;
21; Conservative
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; Pred. No. 74;
0; Mismatches
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Pred. No. 74;
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                US-10-336-603A-11/c
US-10-36-603A-11/c
; Sequence 11, Application US/10336603A
; Publication No. US20040072997A1
; GENERAL INFORMATION:
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APPLICANT: CHERRINGTON, JULIE
APPLICANT: SCHILLING, JIM
APPLICANTON: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
FILE REFERENCE: 038602/1592
CURRENT APPLICATION NUMBER: US/10/440,464
CURRENT FILING DATE: 2003-05-19
PRIOR APPLICATION NUMBER: 60/380,872
PRIOR FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: 60/448,922
PRIOR FILING DATE: 2003-02-24
PRIOR FILING DATE: 2003-02-24
PRIOR FILING DATE: 2003-02-24
NUMBER OF SEQ ID NOS: 185
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 125
LENGTH: 2963
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DATABASE ENTRY DATE: 2003-04-07
RELEVANT RESIDUES: (1)..(2963)
US-10-444-575-5
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Publication No. US20040018528A1
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Best Local Similarity
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Best Local
                                                                          Matches
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AUTHORS: Tobe, T., Saguchi, K., Hashimoto, K., Miura, N.H., Tomita, M.,
AUTHORS: Li, F., Wang, Y., Minoshima, S., and Shimizu, N.
TITLE: Mapping of human inter-alpha-trypsin inhibitor family heavy
TITLE: chain-related protein gene (ITIHL1) to human chromosome 3p21-p14
JOURNAL: Cytogenet. Cell Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: DEPRIMO,
APPLICANT: O'FARREI
APPLICANT: MORIMOTO
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DATE: 1995
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                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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                                                                                            Local Similarity
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1321 CCAGCTTCTCCAGGAAGGCATAGCT
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                                 1 CCAGCATCTCCACGAAGGCAGAGTT 25
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                                                                                            74.48;
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Pred. No. 74;
                                                                          Score 18.6; D
Pred. No. 74;
0; Mismatches
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US-09-880-107-1654/c
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; ORGANISM: Homo sapiens
US-09-964-824A-234
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; LOCATION: (130)..(2829)
US-10-336-603A-11
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                                                                                                                          Sequence 1654, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:
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APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Seate
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-73
CURRENT PAPLICATION NUMBER: US/09/964,824A
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,032
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.0
SEQ ID NO 234
LENGTH: 3058
                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEC.
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    TITLE OF INVENTION:
FILE REFERENCE: 4497
                                            APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/60/236,028
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 169
SOFTWARE: CuraSeqList version 0.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: 21402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2968
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                      1417 CCAGCTTCTCCAGGAAGGCATAGCT 1393
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Similarity 84.0%;
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Vockley, Joseph G.
Scherf, Uwe
Gene Logic, Inc.
VENTION: Gene Expression Profiles in Liver Cancer
NCE: 44921-5028-WO
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Pred. No. 7
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Pred. No. 74;
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PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1654
LENGTH: 3058
TYPE: DNA
PRESENTED NO BAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens FEATURE: ; PEATURE: ; NAME/KEY: CDS ; LOCATION: (130)..(2919) US-10-336-603A-5
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; OTHER INFORMATION: Genbank Accession No. US-09-880-107-1654
                                                                                                                                                                                                 US-10-367-094-71
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; Publication No. US20040170982A1
; GENERAL INFORMATION:
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Best Local S
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APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001500
CURRENT APPLICATION NUMBER: US/10/367,094
CURRENT FILING DATE: 2003-02-14
NUMBER OF SEQ ID NOS: 203
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Best Local (
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PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
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CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
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CURRENT FILING DATE: 2001-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Alsobrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
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; Pred. No. 74;
0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 71

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Sequence 230104, Application US/10027632

| Publication No. US20020198371A1 |
| GENERAL INFORMATION: APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129 |
| CURRENT APPLICATION NUMBER: US/10/027,632 |
| CURRENT APPLICATION NUMBER: US 60/218,006 |
| PRIOR APPLICATION NUMBER: US 60/218,006 |
| PRIOR FILING DATE: 2000-07-12 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR APPLICATION NUMBER: US 60/198,676 |
| PRIOR APPLICATION NUMBER: US 60/193,483 |
| PRIOR APPLICATION NUMBER: US 60/193,483 |
| PRIOR APPLICATION NUMBER: US 60/185,218 |
| PRIOR APPLICATION NUMBER: US 60/167,363 |
| PRIOR APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 494
; TYPE: DNA
; ORGANISM: Human
; 0-10-027-632-230104
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, NAME/KEY: misc_feature
, LOCATION: (1)...(684187)
, OTHER INFORMATION: n = A,T,C or G
US-10-367-094-71
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Search completed: February 9, 2005, 22:26:38 Job time : 268.667 secs
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                                                                                                                                                                                                                                                                                                     Best Local Similarity 87.0 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                           3 AGCATCTCCACGAAGGCAGAGTT 25
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87.0%; Pred. No. 1.2e+02;
ative 0; Mismatches 3;
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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1: geneseqn1980s:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
geneseqn2002as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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25 100.0 25 100.0 26 170.0 27 170.0 28 170.0 29 170.0 20 170.0 20 170.0 21 100.0 21 100.0 22 100.0 23 100.0 24 100.0 25 100.0 26 100.0 27 100	ი	21	2 2 5 5	100.0	2 2 5 5	თ თ	AAD39000 AAD39010
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25 100.0 1 25 100.0 17 25 100.0 17 25 100.0 17 25 100.0 17 25 100.0 17 25 100.0 17 18.6 74.4 118.6 74.4 118.6 74.4 118.6 74.4 118.6 74.4 118.6 74.4	n i	7	25	100.0	8573	6	ABS98184
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18.6 74.4 18.6 74.4 18.6 74.4 18.6 74.4 18.6 74.4	<u>،</u>	4.	18.6	74.4	60	თ	ABN37191
18.6 74.4 18.6 74.4 18.6 74.4 18.6 74.4 18.6 74.4	۰	ហ	18.6	74.4	354	12	ADO44565
.6 74.4 .6 74.4 .6 74.4	o L	<u>,</u>	18.6	74.4	807	10	ADC39482
.6 74.4 .6 74.4 .6 74.4	Ω ·	7	18.6	74.4	867	10	ADE09661
.6 74.4 .6 74.4	o L	60	18.6	74.4	1506	12	ADP28080
.6 74.4	a	ω	18.6	74.4	1506	12	ADP28075
	Ω N	õ	18.6	74.4	2028	11	ABD14475

	C 44		c 42		4.		w	c 37	36	c 35	w	w	w	c 31	w	N	N	N	N	N	N	N	N	c 21	
	18.6 18.2	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6		18.6		18.6	•	18.6	•	18.6	
	72.8	4.	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	
	444 444	5793	5783	5756	5672	4226	4042	3906	3525	3489	3144	3058	3058	3058	3058	2968	2963	2963	2963	2960	2914	2905	2834	2797	
	44 L	13	13	13	13	12	10	11	11	œ	10	10	σ	σ	6	10	12	12	σ	13	10	12	12	10	
ALIGNMENTS	AAI79965	ACN42391	ACN42392	ACN42393	ACN42394	ADQ64433	ADE07449	ABD14647	ABD14104	ACC59960	ADG75752	ADD49032	ABN95156	ABL41972	ABL67200	ADD49038	ADI19055	ADH17126	ABL41971	ACN37942	ADD49036	ADJ72005	ADJ72006	ADD49034	
	Aai79965 Human pol	ACD42391 Human Graf	Human	Human	Human	Novel	Nover	Pseud		ACC59960 Human Prim	Adg75752 Human pro	Add49032 Human NOV					Human					Human	Human	Human	

RESULT 1 AAD3900 ID AAD390 XX AAD3 XX AAD3 XX AAD3 XX AAD3 XX Huma XX Huma XX Huma XX Huma XX Phose XX Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphotid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; antisense; AAD39000; AAD39000 standard; DNA; 25 Human mdr1-HRE antisense oligonucleotide #3. 23-SEP-2002 (first entry) Synthetic. Homo sapiens. modified_base phosphorothicate Location/Qualifiers backbone; ss. ВP

02-MAY-2002. 26-OCT-2000; 2000US-0243542P. 25-OCT-2001; 2001WO-US049856. WO200234291-A2 (BGHM) BRIGHAM & WOMENS HOSPITAL INC. /mod_base= OTHER /note= "Phosphorothioate backbone"

/*tag= a

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

WPI; 2002-471427/50.

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RESULT 2
AAD39010/c
ID AAD390
XX AAD390
XX AAD390
XX Human
AX Human;
KW Hypoxi
PFT Misc_I
PFT S-OC
XX Hypoxi
PFF 25-OC
XX Colga
XX GEGHM
XX Colga
XX WPI;
XX Treat
PFT Treat
PFT Treat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC of developing a haematologic malignancy or multidrug resistance (MDR).

CC The method involves administering hypoxia inducible factor-1 (HIF-1)

CC binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding

CC molecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive

CC element (HRE) binding molecules or antisense nucleic acid molecules and

CC SUMO-1 binding molecules or antisense molecules are useful for treating a

CC (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders

CC (e.g. a lymphoma, myeloma or chronic lymphoproliferative disorders

CC e.g. Lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid

CC disorders include chronic or acute myeloid leukaemia, e.g. angiogenic

CC myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The

CC invention is used in gene therapy. The present sequence is an antisense

CC colgo targetted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its

CC expression. This oligo is used in the exemplification of the invention
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Best Local :
            multidrug resistance, e.g. lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
                                 Treating a subject (at
                                                                    WPI; 2002-471427/50
                                                                                                     Colgan
                                                                                                                                                                            26-OCT-2000;
                                                                                                                                                                                                           25-OCT-2001; 2001WO-US049856
                                                                                                                                                                                                                                                  02-MAY-2002.
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                                                                                                                                                                                                                                                                                                                                                      misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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25; Conserv
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                                                                                                                                         BRIGHAM
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                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                         WOMENS HOSPITAL INC
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            c of) having a
lymphoma or 
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                                                                                                                                                                                                                                                                                                                                                                                                                                           responsive element; HRE;
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Pred. No. 0.1
); Mismatches
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           a hematologic malignancy o myeloma, by administering
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            or
ng hypoxia
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differentiating

invention describes a method for detecting and ring between haematopoietic cell proliferative disorders

Claim 38;

SEQ

ID NO

37; 117pp; English.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

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RESULT 3
ABZ09897/c
ID ABZ098
XX ABZ098
XX ABZ098
XX Human
DT 16-JAN
XX Human;
KW Gene t
KW Gene t
KW Gytosi
XX WO2002
XX WO2002
XX WO2002
XX Homo s
XX Latin
PI Clek j
PI Lewin
PI Schwol
XX Detect
PT discrip
XX Detect
PT discrip
XX Claim
XX Chem
XX Chem
XX Claim
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Best Local
                                                                                                                                                                                                                                                                      Schwope I,
                                                                                                                                                                                                                                                                                           Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               element (HRE) binding molecules or antisense nucleic acid molecules and SUMO-1 binding molecules or antisense molecules are useful for treating subject having or at risk of developing haematologic malignancy or MDR (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders include lymphocytic leukaemia or chronic lymphoproliferative disorders e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia, e.g. angiogenic myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The invention is used in gene thrapy. The present sequence is human mdr1
                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; haematopoietic cell proliferation disorder; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABZ09897;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The method involves administering hypoxia inducible factor-1 (HIF-1) binding molecules or small ubiquitin-like-modifier (SUMO)-1 binding molecules or HIF-1.SUMO-1 complex modulators. mdrl-hypoxia responsive
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, Ziebarth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002WO-EP003401.
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vlation state; gene; ds
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Pred. No.
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1 P, Grabs
Model F,
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                                                                                                                                                                                                                                                                                                            Mueller J;
Leu E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                             to T,
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se (MDR).
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associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present account of the present differentiating between healthy haematopoletic cells and proliferative disorder haematopoletic cells; for differentiating between acute

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RESULT 4

ADB53945/c

ID ADB539

XX ADB539

XX ADB539

XX O4-DEC

XX Colon

XX Colon

XX Colon

XX WCOLON

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Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPB) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon cell;
cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                        Rujan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MDR1 genomic DNA region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003
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                                                                                     Claim
                                                                                                                                     associated with target nucleic a
                                                                                                                                                                       Detecting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2932 BP;
                                                                                                                                    and differentiating between colon cell proliferative disorders d with a gene or its regulatory regions comprises contacting a cleic acid in a biological sample obtained from the subject with
                                                                                                                                                                                                                                         Schmitt A;
                                                                                     SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferative; cancer; adence
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                                                                                     <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ative disorder; non methylated CpG dinucleotide; adenoma; carcinoma; cytosine methylation state;
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                                                                                  74pp;
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Pred. No.
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                                                                                     English.
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                                                                                                                                                                                                                                                             Nimmrich I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.36;
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                                                                                                                                                                                                                                                             Becker
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The invention relates to a novel method for detecting and differentiating between colon cell proliferative disorders associated with at least one gene or its regulatory regions. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at

differentiating

between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CpG dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MDR1, CSNX2B, EGR4, AR, CDK4, RB2, CDC25A, GPID beta, MYCD1, CDH3, MYCL1, ELL1, ABC1, APC, CDH1, CDKN1A, CDKN1B, CDKN2A, CDKN2B, FOS, GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC,

The invention relates to a method of detecting and differentiating

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RESULT 5
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XX ds; ly
KW methyl
KW diffus
KW chroni
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XX Homo s
XX 25-NOV
PR 23-NOV
PR 23-NOV
PR 28-DEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; mingle nucleotide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5' regulatory region of human gene MDR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                               Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least reagent that distinguishes between methylated and non-methylated Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 follicular lymphoma;
                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 1; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-457621/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-2001;
28-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caldwell C,
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2001DE-01064501.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 25;
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The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSK3beta, ESR1, APAF1, BAK1, BAX or HOXA5. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the cpG dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular lymphoma. They are also useful for detecting of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treating and/or menitoring of lymphoid cell proliferative disorder. This sequence represents the 5' and/or regulatory region from one of the above
                                                                                                                                                                                                                  Predicting responsiveness of a subject with breast cell disorder, useful for treating or differentiating breast proliferative disorders comprises analyzing methylation
                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002; 2002DE-01045779.
07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
                                                                                                                                                                     Example 2;
                                                                                                                                                                                                     genomic
                                                                                                                                                                                                                                                                                      WPI; 2004-348468/32.
                                                                                                                                                                                                                                                                                                                       Nimmrich
                                                                                                                                                                                                                                                                                                                                     Foekens J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003; 2003WO-EP010881.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004035803-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADS88985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCATCTCCACGAAGGCAGAGTT 25
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                                                                                                                                                                   SEQ ID NO 1; 104pp; English.
                                                                                                                                                                                                                                                                                                                    Harbeck N,
Rujan T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell proliferative disorder; breast; methylation; therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                      ΑG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                     subject.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; 564 C;
                                                                                                                                                                                                                                                                                                                     Koenig
Schmitt
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Pred. No. 0
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Schmitt |
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                                                                                                                                                                                                                  cell
pattern of a
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Marx A;
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RESULT 7
ABS98184/c
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                                                                                                 Query Match
Best Local S
Matches 25
                                                                                                                                                                          treatment, characterisation, classification and/or differentiation, observed that the method is also useful for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy. The present sequence is in the exemplification of the invention.
                                                                                                                                                     Sequence 2932 BP;
                                                                                                                                                                                                                                        methods, nucleic acid, oligonucleotide,
                                                                                                    25;
                                                                                                                Similarity
                                                                   CCAGCATCTCCACGAAGGCAGAGTT
                                                   CCAGCATCTCCACGAAGGCAGAGTT 1570
                                                                                                  100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                   841 A; 564 C; 653
                                                                                                  0;
                                                                                                              Score 25;
Pred. No.
                                                                                                    Mismatches
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                                                                                                                          Length 2932;
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                                                                                                                                                     Other;
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                                                                                                  Gaps
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Human; ds; cytochrome P450 A1; CYP4501A1; UGT2B4; MDR1;

KW cytochrome P450 A2; CYP4501A2; cytochrome P450 02E; CYP4502E1; LTF;

KW adrenergic receptor beta1; ADBR1; aryl hydrocarbon; ARNI; CATHABIN S; CTSS;

KW aryl hydrocarbon receptor nuclear translocator; ARNI; cathapsin S; CTSS;

KW cyclooxgenase 2; COX2; diazepam binding inhibitor; DBI; haematological;

KW cyclooxyenase 2; EPHX2; 5-lipoxygenase activating protein; FLAP;

KW diathione-S-transferase 12; GST12; histamine-N-methyl transferase;

KW HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase; NNMT;

KW HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase 2NM;

KW HMMT; kallikrein 2; KLK2; nicotinamide-N-methyl transferase 2NM;

KW HMDPH quinone oxidoreductase 21; NQO2; sulfotransferase thermolabile; STM;

KW UDP-glucuronosyl transferase 2NM; UDP-glucuronosyl transferase 2NM;

KW UDP-glucuronosyl transferase; NGO2; sulfotransferase 2NM;

KW UDP-glucuronosyl transferase; NGO2; sulfotransferase 2NM;

KW UDP-glucuronosyl transferase; NGO2; sulfotransferase; uPA;

KW UDP-glucuronosyl transferase; NGT2B15; urokinase receptor; uPA;

KW udlidrug resistance associated protesin 3; caneer; protestate;

KW acetylcholine muscarinic receptor; CHMR1; CHMR2; CHMR4; CHMR5;

Altered drug metabolism; cardiovascular function; colorectal tumour;

KW central nervous system; nulmonary; immunological; SUNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human multidrug resistance
                               altered drug metabolism; cardiovascular function; colorectal tumour; central nervous system; pulmonary; immunological; SNP;
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nucleotide
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polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene promoter B and exons 1-3 sequence
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WO200257410-A2

25-JUL-2002

28-NOV-2001; 2001WO-US044838.

28-NOV-2000; 2000US-00724389

(DNAS-) DNA SCI LAB

Guida z, ۲,

2002-698522/75

Isolated nucleic acid molecules having polymorphisms in known human genetic cytochrome p450 and cathepsin S useful as genetic linkage markers for locating, identifying and characterizing the genes responsible for disorder-related traits.

Page 432-437; 714pp; English

This invention relates to the sequence of an iso molecule comprising at least one base variation human cytochrome P450 A1 (CYP450A1), cytochrome cytochrome P450 02E1 (CYP45002E1), adrenergic re variation from that of a known cytochrome P450 A2 (CYP4501A2) isolated receptor nucleic

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RESULT 8
ADD41243/c
ID AADD412
XX AAD412
XX AAD412
XX AAD412
XX AAD412
XX Human;
KW LTAING
KW P-glyc
XX P-glyc
XX Homo 8
XX WO2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aryl hydrocarbon (AHR), aryl hydrocarbon receptor nuclear translocator (ARNY), cathepsin S (CTSS), cyclooxgenase 2 (COX2), diazepam binding inhibitor (DBI), epoxide hydroxylase 2 (EPHX2), 5-lipoxygenase activating protein (FLAP), glutathione-S-transferase 12 (GST12), histamine-N-methyl transferase (HNMT), (kallikrein 2) KLK2, nicotinamide -N-methyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; transgenic; reporter construct; CYP3A4; cytochrome transcriptional regulatory element; xenobiotic; steroid; Pglycoprotein; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8573 BP; 2739 A; 1422 C; 1705 G;
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Liddle C,
                                                                                                                                   01-NOV-2000;
10-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human MDR1 gene 5' flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-OCT-2002
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                                                                   (UNSY ) UNIV SYDNEY
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       Goodwin BJ,
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                                                                                                                                   2000AU-00001161
2001AU-00004901
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       Robertson
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RESULT 9
ACF62751/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to generation of non-human transgenic animals comprising a reporter construct for producing a detectable amount of a reporter molecule operably linked to a transcriptional regulatory nucleic acid molecule from the human CYP3A4 gene. The invention also relates to transgenic animal for analysing CYP3A4 cytochrome P450 gene regulation. The non-human mammal of the invention is useful for determining whether a compound is capable of effecting the transcription of a human CYP3A4 gene. It is also useful for determining the effect of a compound such as a xenobiotic or steroid on the regulation of expression of the CYP3A4 gene in a human. The present sequence is 5' flanking region of human (p-glycoprotein) MDR1 gene. This sequence is used as a regulatory element in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-human mammal for determining the effect of a compound on regulation of CYP3A4 gene expression, comprises a reporter construct for producing reporter linked to a transcriptional regulatory nucleic acid from a hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-537301/57.
                                                                                                                                                                                                                                                                                                                                                                                Cancer; CYP3A5; irinotecan; pharmaceutical; malignant glioma;
cytochrome p450; subfamily IIIA; nifedipine oxidase; polypeptide 5;
cytostatic; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10200 BP; 3296 A; 1785 C; 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Cancer based on CYP3A5 related polynucleotide SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACF62751
                                                                   New use of irinotecan for preparation of compositions for treating in subject having genome with variant allele comprising cytochrome subfamily IIIA, polypeptide 5 polynucleotide, termed CYP3A5.
                                                                                                                                                                                                                   23-JUL-2001; 2001EP-00117608.
24-MAY-2002; 2002EP-00011710.
                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                               WPI; 2003-268144/26.
                                                                                                                                                            Heinrich G,
                                                                                                                                                                                                                                                                 23-JUL-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGCATCTCCACGAAGGCAGAGTT 9793
                                          SEQ
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                                                                                                                                                            Kerb
                                                                                                                                                                                                                                                                 2002WO-EP008219
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                                          ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 177380
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100.0%; Pred. No.
                                            683;
                                          : dd98
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                                          English.
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                                                                                        p450,
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The present invention describes the use of irinotecan (I) or its derivative for the preparation of a pharmaceutical composition for

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RESULT 10
ADB20870/c
ID ADB208
XX ADB208
XX ADB208
XX ININCT
DT 20-NOV
XX irinot
KW irinot
KW Lung c
KW varian
KW Varian
KW Varian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a cytochrome p450, subfamily IIIA (nifedipine oxidase), polypeptide 5 (CYPAS) polynucleotide (II). (I) and (II) have cytostatic activity. The therapeutic applications of (I) is improved, since it is possible to individually treat a subject with an appropriate desirvative of (I). Therefore, undesirable, harmful or toxic effects are efficiently avoided. Unnecessary and potentially harmful treatment of those subjects who do not respond to the treatment with substances (nonresponders), as well as the development of drug resistances due to suboptimal drug dosing can be avoided. ACF62200 to ACF62751 and ABM34912 to ABM35013 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                     Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1
                                                                                                                                                                                                                                                                                                                                                                                  23-JUL-2001;
24-MAY-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       irinotecan; colorectal cancer; cervical cancer; gastric cancer;
lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
variant allele; multidrug resistance protein 1; MRP1; cytostatic;
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2002EP-00011710.
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Pred. No. 0.6
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The present invention describes a method for the use of irinotecan (I) of its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance protein 1 (MRP1) polynucleotide (II). (I) has cytostatic activity. (I) or its derivative can be used for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject, where the subject is a human

Disclosure; SEQ ID NO 683; 100pp; English

or P

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CCAGCATCTCCACGAAGGCAGAGTT

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Query Match Best Local (Matches

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                                              The invention relates to the novel use of irinotecan to treat a patient suffering from cancer. This involves determining if the patient has one or more variant alleles of the UGTIA1 gene, and if the patient has one or more of such variant alleles, irinotecan is administered in an increased or decreased amount in comparison to the amount that is administered without regard to the patient's alleles in the UGTIA1 gene. The invention has cytostatic activity. A composition of the invention acts as a topoisomerase I inhibitor. The method is useful for treating a patient, an animal e.g. mouse or a human, preferably African or Asian, suffering from cancer such as colorectal, cervical, gastric cancer, lung, ovarian, pancreatic cancer or malignant glioma. The present sequence is udes in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of irinotecan to treat cancer patient by determining if patient has variant alleles of UGT1A1 gene, administering increased/decreased amounts of irinotecan based on increased/decreased levels of UGT1A1 gene product.
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24-MAY-2002;
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2002EP-00011710.
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; human; Cyp3A5; MRP1; MDR1;
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24-MAY-2002; 2002EP-00011710.
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      Human MDR1
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100.0%; Pred. No. 0.0
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RESULT 14
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Matches 25
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; human; UGTIA1; MRP1; TOP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates ro a novel use of irinotecan or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The present sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUL-2001; 2001EP-00117608.
24-MAY-2002; 2002EP-00011710.
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                                                                                                                                                                       Human;
splice
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                    ABN37191 standard; DNA; 60 BP
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                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                    15-JUL-2002
                                                                                                                                                                                                                                                             ABN37191;
                                 28-JUL-2000; 2000US-0221607P.
02-MAY-2001; 2001US-0287724P.
                                                                      20-JUL-2001; 2001WO-IB001903
                                                                                                07-FEB-2002
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variant;
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25; Conserv
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                         rat; splice transcript; detection; RNA transcript; t; transcriptome; oligonucleotide library; ss.
                                                                                                                                                                                                          transcript detection oligonucleotide SEQ ID NO:9939
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(COMP-) COMPUGEN INC

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RESULT 15
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XX AD044
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XX CRH;
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                                                                                                                                                         31-OCT-2002; 2002WO-EP012274
                                                                                                                                                                                                                        23-OCT-2003; 2003WO-EP011792
                                                                                                                                                                                                                                                                                           13-MAY-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRH; corticotropin-releasing hormone; antidepressant; tranquillizer; gene therapy; CNS; expressed sequence tag; EST; ds.
   Fierens
                                 Peeters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 60 BP; 16 A; 15 C; 16 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of
                                                                                                (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI480570expressed sequence tag (EST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoshan A,
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                                 Goehlmann HWH,
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Pred. No. 1.6e
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Diagnosing a corticotropin-releasing hormone (CRH)-induced gene expression profile in an individual comprises determining polypeptides and polynucleotides that mediate the endocrine response to CRH in the
                                                                                                                                          Claim 1; SEQ ID NO 31; 84pp; English.
                                                                                                                                                             sample
                                                                                                                                                                                                      GENBANK; AI848545.
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The invention relates to diagnosing a corticotropin-releasing hormone (CRH)-induced gene expression profile in an individual. The method involves determining the level of gene transcription of a gene comprising a nucleic acid sequence selected from 28 nucleotide sequences fully defined in the specification or determining the amount of at least one protein that modulates CRH signaling in the sample, where the protein comprises 13 amino acid sequences given in the specification. The methods and composition are useful for diagnosing, treating and/or preventing CRH metabolism-related disorders, such as CRH-induced depression or stress. The polymucleotide is used as a marker of CRH signaling in a cell. These composition and methods may also be used in identifying compounds that modulate CRH-induced depression and stress. The present sequence represents a specific example of a gene fragment that is an important mediator of CRH-induced changes in the CNS.

Sequence 354 BP; 107 A; 71 C; 68 G; 108 T; 0 U; 0 Other;

Ś Query Match Best Local S Matches 21 1 CCAGCATCTCCACGAAGGCAGAGTT 25 21; Similarity Conservative 74.4%; 84.0%; 0; Score 18.6; DB Pred. No. 2e+02; O; Mismatches 12; 4. Length Indels 0 Gaps

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Search comp Job time : 맑 completed: February me : 247.69 secs 262 CCAGCAGCTCCACGAAGTCAGTGAT 286 9, 2005, 16:05:56

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Title:
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Match
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25
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Gapop 10.0 , Gapext 1.0
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gb_est2:*
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9b est4:
9b est5: *
9b est6: *
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 AV631826
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CCG206154
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AV631826 AV631826

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BZ536972 OGAHHISTC

CG206154 PUJDB60TD

CG436506 CGVCB10TH

BZ785280 PUFAX84TB

CG436517 OGVGE10TV

BM257699 521522 MA

ALT26135 ALT26135

BX307891 BX307891

BX29583 BX307891

AV59429 BX299583

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CR364140 CR364140

CR364140 
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ALIGNMENTS

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Db 47	Qy	Query Match Best Local : Matches 2:	ORIGIN							source	FEATURES			COMMENT	PUBMED	MEDLINE	JOURNAL	BTLLE	3	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	2		DEFINITION	826	RESULT 1
74 CCAGCATCTTCACAAATGCAGAGTT 498	1 CCAGCATCTCCACGAAGGCAGAGTT 25	y Match 80.8%; Score 20.2; DB 1; Length 505; Local Similarity 88.0%; Pred. No. 4.1e+02; hes 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		5% to 0.04%"	.XhoI; The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from	<pre>/clone_lib="Chlamydomonas reinhardtii 5% to 0.04% CO2" /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:</pre>	/db_xrer="taxon:3055" /clone="LCL100d12_r"	/mor_cype="mxxxx" /strain="C9"	/organism="Chlamydomonas reinhardtii"	1505	Location/Qualifiers	Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Rmail: asamizu@kazusa.or.ip. URL:http://www.kazusa.or.ip/en/plant/.	Kazusa DNA Research Institute	Contact: Erika Asamizu	11089912		DNA Res. 7 (5), 305-307 (2000)	Generation of expressed sequence tags from fow-to- and high-to-	low-cos and	Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K.,	to 505)	Eukaryota; viriqipiantae; chiorophyta; chiorophyteae; voivotaies; Chlamydomonadaceae; Chlamydomonas.	reinhardtii	Chlamydomonas reinhardtii	ç	AV631826 1 GT-10794460	LCL100d12_r 5', mRNA sequent	AV631826 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas		

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AUTHORS
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BZ536972
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AV626483
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                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 702)

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                        OGAHH18TC ZM2_0.7_1.5_KB genomic survey sequence. BZ536972
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Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from
adapted cells of Chlamydomonas reinhardtii
DDAR. Res. 7 (5), 305-307 (2000)
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Bukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
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                                                                                                                                                                                                                                                             Zea mays
                                                                                                                                                                                                                                                                                                                      BZ536972.1 GI:27085170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 514)
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                        Medical Center Drive,
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/clone="LCL099h12 r"
/clone="LCL099h12 r"
/clone=11b="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/clone 11b="Chlamydomonas reinhardtii 5% to 0.04% CO2"
/note="Vector: pBluescriptII SK-; Site 1: EcoRI; Site 2:
XhOI; The cDNA library was constructed from cells cultured in a carbon stress acclimatized condition in which carbon dioxide concentration in the bubbling gas was changed from 5% to 0.04%"
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Zea
                        Rockville,
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                        20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 514;
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Best Local Similarity
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367
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CG206154
CG206154.1 GI:3
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                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive,
Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2003)
Other_GSSs: PUJDB60TB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. an
                                                                                                                                                                                                                                                                                                                                                                                      Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                               Resnick,A., Fraser,C.M.,
Bennetzen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301-838-5843
                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 301-838-0208
                          CCAGCATCTCCACGAAGGCAGAGTT
CCAGCATCTGCACGGAGGCAAAGTT
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                                                                                                                            /clone="ZMMBTa0640J24"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site_1:
CoT selected genomic DNA library"
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/clone lib="ZM2_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.
methylation filtered genomic DNA library"
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'strain="B73"
                                                                                                                                                                                                                                    organism="Zea mays"
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/strain="B73"
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/mol_type="genomic D
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                                                                                                                                                                                            _xref="taxon:4577"
                                                                     80.8%;
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Pred. No. 4.3e+02;
0; Mismatches 3
                                                         Score 20.2; DB 9;
Pred. No. 4.3e+02;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea
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                           25
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a; Poales; Poaceae; PACCAD
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CG436506
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                                      COMMENT
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Best Local Similarity
Matches 22; Conserv
                                                      TITLE
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1 (bases 1 to 852)

1 (bases 1 to, 852)

1 (bases 1, Mackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Robitas, Bedell, J.A., Rohlfing, T., Reprick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CG436506 852 bp DNA linear GSS 17-SEP-2003
OGVGE10TH ZM 0.7_1.5_KB Zea mays genomic clone ZMMBMa0475A19,
genomic survey sequence.
CG436506
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Other_GSSs: OGVGE10TV
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                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 893)

whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Whitelaw,C.A., Traser,C.M., Yuan,Y., San Miguel,P., Ma,J. and Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                                                                                                                                                                                                                                                                              genomic survey sequence.
BZ785280
BZ785280.1 GI:28978877
GSS.
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PUFAX84TB ZM_0.6_1.0_KB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Cathy Whitelaw
                                   Contact: Cathy Whitelaw
                                                      Maize Genomics Consortium 
Unpublished (2003)
                                                                                                                                                                                                                                      Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301-838-0208
9712 Medical Center Drive, Rockville, MD 20850, USA
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/mol type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="EaxMBMA0475A19"
/clone="ZMMBMA0475A19"
/clone="EaxMEMA0475A19"
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/clone="EaxMEMA0475A19"
/clone="EaxMEMA0475A19"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5
methylation filtered genomic DNA library"
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Best Local S
Matches 22
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JOURNAL
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Matches 22; Conserv
                                                                                       Query Match
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Class: sheared ends.
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Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 955)

whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)
Other_GSSs: OGVGE10TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
CG436517
CG436517.1 GI:34813056
GSS.
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Tel: 301-838-5843
Fax: 301-838-0208
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                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                       Seq primer: TF
                                                                                                                                                                                                                                                                                                                        Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAGCATCTGCACGGAGGCAAAGTT 391
 CCAGCATCTGCACGGAGGCAAAGTT
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/clone="b="ZM,06f.0 KB"
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CoT selected genomic DNA library"
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/mol_type="genomic D
/strain="B73"
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                                                                                                                                    /clone="ZMMBMa0475A19"
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/notee="Vettor: pBCSK-; Site 1:
methylation filtered genomic DN
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                                                           Score 20.2; DB 9;
Pred. No. 4.5e+02;
0; Mismatches 3;
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BM257699/c
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Best Local S
Matches 21
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MEDLINE
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AL726135.1
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AL726135 Danio rerio embryonic inner ear subtracted rerio CDNA clone BNOAA083ZH02 5', mRNA sequence.
                                    Danio rerio (zebrafish)
Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 550)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F., Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, G., Liang, F., Chitko-McKown, C.G., Pertea, G., Chitko-McKown, C.G., Chitko-McKown, C.G., Chitko-McKown, C.G., Chitko-McKown, C.G., Chitko-McKown, C.G., Chitko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 125 row: D column: 5
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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BACKWARD: GTTTTCCCAGTCACGACG
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BM257699 550 bp mRNA linear 521522 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
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/lab_hosf="DH10B"
/clone_lib="MARC_3BOV"
/note="Vector: pCMV_SPORT6; Site_1: NotI; Site_1
Library_made_from_pooled_tissue_from_marrow, almacrophage, ovary, fetal_semitendonosus_muscle, longissimus_muscle."
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/mol_type="mRNA"
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Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                         GI:20190739
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91.3%;
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Pred. No. 6.2e+02;
0; Mismatches 2
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CDNA Danio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299
                                                                                                                                                                                                                                       Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and re
at sigenasupport@jouy.inra.fr to obtain the
                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29588536.
Contact: Guiguen Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W
                                                                                                                                                                                                     sequence.
Plate: 0016
                                                                                                                                                                                                                                                                                                  Campus de beaulieu,
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                   Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA
Libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 585)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncorhynchus mykiss (rainbow trout) Oncorhynchus mykiss
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BX307891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex
Email: segref@genoscope.rus.fr, Web : www.genoscop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 584)
Coimbra,R., Weil,D., Brottier,P., Blanchard,S., Levi, Hardelin,J.P., Weissenbach,J. and Petit,C.
A subtracted cDNA library from the zebrafish (Danio r
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Unpublished (2002)
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/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="texon:8022"
/clone="tcay0016b.m.17"
/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intest
kidney, liver, muscle, ovary, pituitary, testis"
                                                                                                                                                               Location/Qualifiers
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/dev_stage="embryonic"
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/mol_type="mRNA"
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Pred. No. 6.3e+02;
0; Mismatches 2
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AL726201/c
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AV594929/c
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1 (bases 1 to 587)

1 (coimbra, R., Weil, D., Brottler, P., Blanchard, S., Hardelin, J.P., Weissenbach, J. and Petit, C.

A subtracted cDNA library from the zebrafish (Dz.)
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rerio cDNA clone BNOAA083ZH02
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AV594929 595 b
AV594929 Bos taurus cartilage
E1CA016F04 5', mRNA sequence.
AV594929
AV594929.1 GI:9711387
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex -
Email: seqref@genoscope.cns.fr, Web : www.genoscope
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Unpublished (2002)
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/note="Vector: pT/T3D-pac; Rainbow trout multi-tissues .
/note="Vector: pt/T3D-pac; Rainbo
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/lab_host="DH10B"
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/tissue_type="inner ear"
/dev_stage="embryonic"
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'mol_type="mRNA"
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91.3%;
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Pred. No. 6.3e+02;
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Pred. No. 6.3e+02;
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                                                                                           Bos taurus cDNA
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                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
BX299583/c
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                223
                                INRA - SCRIBE
Campus de beaulieu, l
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fuk
Tel: 81-248-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Establishment of a high throughput EST spoly(A) tail-removed cDNA libraries and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Sugimoto, Y.
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing.
This clone was obtained from a polyA-deleted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 81-248-25-5725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Yoshikazu Sugimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bovine ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Takasuga, A., Hirotsune, S., Itoh, R., Jitohzono, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                      Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29580228.
                                                                                                                                                         Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                   Oncorhynchus mykiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kazusugi@cocoa.ocn.ne.jp
                                                                                                                                                                                                                                                                                                  Oncorhynchus mykiss (rainbow trout)
                                                                                                                                                                                                                                                                                                                                       BX299583.2
                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
                                                                                                          Contact: Guiguen Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGCATCTCCACGAAGGCAGAG 23
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                                                                                                                                                                                                            (bases 1 to 680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="Bos taurus cartilage fetus"
/note="Vector: pZL1; Site 1: Sal1; Site
was deleted from a Not1 sIte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="cartilage"
/dev_stage="fetus"
/lab_host="DH10B"
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/clone="E1CA016F04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Bos taurus"
/mol_type="mRNA"
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                                                                       RENNES
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Pred. No. 6.3e+02;
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tcay0004b.i.10 5prim,
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tion of 36,000
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CR364140/c
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0038,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campus de beaulieu, RENNES cedex, Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Construction and primary characterization of normalized cDNA libraries in rainbow trout, Oncorhynchus mykiss Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus. 1 (bases 1 to 687)
Govoroun, M., Guiguen, Y. and Le Gac, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CR364140 687 bp mRNA linear EST 21-APR-2004 CR364140 AGENAE Rainbow trout normalized testis library (tcbi) Oncorhynchus mykiss cDNA clone tcbi0038c.j.24 Sprim, mRNA sequence. CR364140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at sigenasupport@jouy.inra.fr to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and re
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                                                                                             /organism="Oncorhynchus m
/mol type="mRNA"
/db xref="texon:8022"
/clone="texi0038c.j.24"
/tissue_type="testis"
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/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues .
/note="Vector: pT7T3D-pac; Rainbo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intest
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="AGENAE Rainbow trout
(tcbi)"
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                                                                          lab host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcay0004b.i.10"
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Pred. No. 6.4e+02;
0; Mismatches 2;
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                           normalized testis library
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646 CCAGCACCTCCACGAATGCAGAG
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                                                            21;
                                                                                                                                                                                                                                                                         Email: srvoss@uky.edu
The EST is quality trimmed at the ends with a 20 base window and
quality threshold of 15 (phred quality score).Please visit
http://salamander.uky.edu For any information(trace,quality files
etc) regarding this EST.
                                                                                                                                                                                                                                                                                                                                                 Department of Biology
University of Kentucky
TH Morgan Building, Lexington,
Tel: 859 257 9888
Fax: 859 257 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
CN069432
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BMC Genomics 5 (1), 54 (
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Ambystoma tigrinum tigrinum
Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: SR Voss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putta,S., Smith,J.J., Walker,J.A., Rondet,M., Weisrock,D., Monaghan,J., Samuels,A.K., Kump,K., King,D.C., Maness,N.J., Habermann,B., Tanaka,E., Bryant,S.V., Gardiner,D.M., Parichy,D.M.
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                                                                         Similarity
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                                                            Conservative
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                                                                                                                                   /mol_type="mRNA"
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/tissue_type="Liver, Lung, Ki
gill tissues collected from m
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                                                                        79.2%;
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91.3%;
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                                                         Score 19.8; DB 7;
Pred. No. 6.6e+02;
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                                                                                                                                                                                                                              tigrinum
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Search completed: February Job time: 2451.85 secs

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2: gb hg:*
2: gb ng:*
3: gb n:*
5: gb om:*
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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CQ315831 Sequence
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CQ219138 Sequence
CQ219138 Sequence
                                                                                                                                                                                                                           Description
   SOURCE
ORGANISM
                         KEYWORDS
  Homo sapiens (human)
Homo sapiens
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RESULT 2 AX504326/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	do Qy	Query Matc Best Local Matches	AUTHORS TITLE JOURNAL FEATURES BOUICE ORIGIN	4 OI	RESULT 1 AX504309 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
AX504326 25 bp DNA Sequence 29 from Patent WO0234291. AX504326 AX504326.1 GI:23386138	1 AGCTTCCAACCACGTGTAAATCCTA 25 	ch 100.0%; Score 25; DB 6; I Similarity 100.0%; Pred. No. 0.059; 25; Conservative 0; Mismatches 0	and methods for treating hig resistance gg resistance 1234291-A 12 02-MAY-2002; AND WOMEN'S HOSPITAL, INC. ation/Qualifiers .25 .25 .25 .25 .25 .25 .25 .25 .25 .27 .27 .28 .28 .29 .29 .28 .29 .29 .28 .29 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .28 .29 .20 .20 .20 .20 .20 .20 .20 .20 .20 .20	omo sapiens (human) omo sapiens ukaryota; Metazoa; Chordata; Craniata; ummalia; Butheria; Primates; Catarrhini	AX504309 25 bp DNA Sequence 12 from Patent WO0234291. AX504309 7 AX504309.1 GI:23386127	ALIGNMENTS	25 100.0 463 6 CQ331579 25 100.0 473 6 CQ236561 25 100.0 473 6 CQ235678 25 100.0 473 6 CQ235678 25 100.0 807 6 I0856 25 100.0 807 6 I0856 25 100.0 3847 6 AX363343 25 100.0 3840 6 AX481416 25 100.0 3852 9 AF537134 25 100.0 3860 6 AX322787 25 100.0 3860 6 AX322787 25 100.0 3988 6 AX322789 25 100.0 3988 6 AX322789 25 100.0 4186 6 AX322789 25 100.0 4186 6 AX399194 25 100.0 4186 6 AX399195 25 100.0 4195 6 AX518654 25 100.0 4195 6 AX518656 25 100.0 4195 6 AR051647 25 100.0 4264 6 AR051650 25 100.0 4264 6 AR051650 25 100.0 4264 6 AR051650 25 100.0 4553 6 CQ716151
linear PAT 27-SEP-2002		Length 25;); Indels 0; Gaps 0;	ematologic malignancies and (US)	Vertebrata; Euteleostomi; .; Hominidae; Homo.	linear PAT 27-SEP-2002		CQ331579 Sequence CQ136561 Sequence CQ235278 Sequence CQ332256 Sequence 108556 Sequence 108557134 Sequence 108571134 Macaca fa 105537134 Macaca fa 105537134 Macaca fa 105537134 Macaca fa 10552789 Sequence 10510394 Macaca mu 10532789 Sequence 10510394 Phosphati 10645256 Sequence 10510474 Sequence 10510474 Sequence 10510474 Sequence 105116475 Sequence

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RESULT 4
BD160756
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Best Local Similarity
Matches 25; Conserv
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synthetic construct
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Patent: WO 0234291-A 29 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
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Mammalia; Eutheria;
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llarity 100.0%;
Conservative 0;
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                                                                                                                                                                                                                                               /organism='Artificial Location/Qualifiers
                                                                                                                                                                                                     /organism="synthetic construct"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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tive 0;
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CQ148922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 100.0%;
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/noTe="MAP TO AC005068.1-EXPLUE 3.00e-27-NT HIT:
AF016535.1, EVALUE 2.00e-92~EST_HUMAN HIT: AW847648.1,
EVALUE 2.30e+00"
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/mol_type="genomic DNA"
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Pred. No. 0.055;
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CQ148922
ch 100.0%;
l Similarity 100.0%;
25; Conservative 0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                         /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/noTe="MAP TO AC005068 1.~EXPRESSED IN ADULT LIVER, SIGNAL 0.73_NT HIT: AF016535.1, EVALUE 2.00e-92~SWISSPROT HIT: P08183, EVALUE 3.00e-27~EST_HUMAN HIT: AM847648.1, EVALUE 2.30e+00"
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/db xref="taxon:9606",
/db xref="taxon:9606",
/note="MAP TO AC005068.1~EXPRESSED IN BONE MARROW, SIGNAL
= 0.53~SWISSPROT HIT: P08183, EVALUE 3.00e-27~NT HIT:
aF01535.1, EVALUE 2.00e-92~EST_HUMAN HIT: AW847648.1,
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CQ307508
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ch 100.0%; l Similarity 100.0%; 25; Conservative (
                                                                                                                                                                                                                            Human genome-derived single exon nucleic acid analysis of gene expression in human brain Patent: WO 0157275-A 18468 09-AUG-2001;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/note="MAP TO AC005068.1-EXPRESSED IN LUNG, SIGNAL = 0.65-SWISSPROT HIT: P08183, EVALUE 3.00e-27-NT HIT: AF016535.1, EVALUE 2.00e-92-EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00"
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/db_xref="taxon:9606"
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                                                       Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M., Cantor,C.R. and Braun,A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
                                                                                                                                                                                                                                  tagged site.
BV202142
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Contact: Andreas Braur
                                 Genome Res.
                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 201)
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
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Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
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3595 John Hopkins Court, San Diego,
Tel: 18582029018
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sqnm208303 Human DNA (Sequenom)
tagged site.
BV202141
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Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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<1...>201
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100.0%; Pred. No. 0.055;
vative 0; Mismatches
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1 (bases 1 to 209)

Gekeler, V., Weger, S. and Probst, H.

mdr1/P-glycoprotein gene segments analyzed from various human leukemic cell lines exhibiting different multidrug resistance
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycoprotein.
2 of 3
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3595 John Hopkins Court, San Diego,
Tel: 18582029018
Fax: 18582029020
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Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
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                                                                                                                                                                                                        /note="glycoprotein intron
complement(1, .19)
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CQ149621/c
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                                                                                                                                                                                                                                                                                                         219 bp DNA
Sequence 19326 from Patent W00186003.
CQ308221
CQ308221.1 GI:41268798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Similarity 100.0%; Pred. No.
25; Conservative 0; Mismatch
                                                                                                                                           Human genome-derived single exon nucleic acid snalysis of gene expression in human lung patent; WO 0186003-A 19326 15-NOV-2001;
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Search completed: February Job time : 483.178 secs

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Sequence 191
CQ345026
CQ345026.1
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                                                                                                                                                                                                                                                           Human genome-derived single exon nucleic acid analysis of gene expression in human brain patent: WO 0157275-A 19120 09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        Similarity
25; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                           Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
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                            AGCTTCCAACCACGTGTAAATCCTA 25
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                                                     100.0%; Score 25; DB 6; ilarity 100.0%; Pred. No. 0.055; Conservative 0; Mismatches
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19120 from Patent WO0157275.
                                                                                                                             /organism="Homo_sapiens"
/mol_type="unassigned_DNA"
/db_xrcf="taxon:9606"
/db_xrcf="taxon:9606"
/note="Map TO AC002457.1-EXPRESSED IN BRAIN, SIGNA
0.57-NT HIT: M29428.1, EVALUE 1.00e-120~SWISSPROT
P08183, EVALUE 2.00e-27"
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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RESULT 1
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TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA ; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS ; NUMBER OF SEQUENCES: 4
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5206352-1
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TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
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APPLICANT: Roninson,
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LENGTH: 807
                SEQ ID NO:1:
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                    APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
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FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                     APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
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US-09-949-016-71318
US-09-949-016-179555
US-09-949-016-179556
US-09-949-016-1795664
US-09-949-016-11437
US-09-949-016-15879
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US-09-949-016-30006
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12437, A
11935, A
16921, A
17533, A
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1
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                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 4186
TYPE: DNA
          Best Loc
Matches
        Query Match 100.0%; Score 25; DB 4; Length 4186; Best Local Similarity 100.0%; Pred. No. 0.0097; Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                     FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
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APPLICANT: Stremmel, Wolfgang
TITLE OF INVENTION: Phosphatidylcholine as Medication with
TITLE OF INVENTION: Protective Effect on Large Intestinal
FILE REFERENCE: 34691/208520
CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                JENERAL INFORMATION:
APPLICANT: STEUMEL-CRESPI, DO:
APPLICANT: STEUMEL-CRESPI, DO:
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP99702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-18-08
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
PRIOR FILING DATE: 1998-12-15
                                                                                                     NAME/KEY: CDS
LOCATION: (100)...(3940)
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; NAME/KEY: CDS
; LOCATION: (100)...(3949)
US-09-672-810-3
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SOFTWARE: PATENTIN Release #1.0, Versio CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/784,649A FILING DATE: CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION: NAME: Sherwood, Pamela J REGISTRATION NUMBER: REGISTRATION NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Macaca fascicularis
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 4195
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO TITLE OF INVENTION: CYCLOSPORIN MODULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sikic APPLICANT: Chen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                   CITY: Menlo Park
                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749
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Chen, Gang
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Version #1.25

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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.
                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR TILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STOCKER, PENNY J.

APPLICANT: STEIMEL-CRESPI, DOROTHY T.

APPLICANT: CRESPI, CHARLES L.

TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               740 AGCTTCCAACCACGTGTAAATCCTA 716
                             1 AGCTTCCAACCACGTGTAAATCCTA 25
AGCTTCCAACCACGTGTAAATCCTA 725
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                                                                                                         Score 25; DB 4;
Pred. No. 0.0098;
                                                                                       Mismatches
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                RESULT 8
US-08-181-471-2/c
                                                                                                                                                                                                                           US-08-784-649A-5
                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 4264 bass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/08784649A
Patent No. 5830697
GENERAL INFORMATION:
APPLICANT: Sikic, Branimir I
APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
Sequence 2, Application US/08181471
                                                                                                                                                     Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: REG.NO. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
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                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson STREET: 2200 Sand Hill Road CITY: Menlo Park
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                                                                                                                                                                                                                                                            STRANDEDNESS:
TOPOLOGY: lir
                                                                                                                                                                                                                                                                                              LENGTH: 4264 base pairs
TYPE: nucleic acid
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                                                                                                                                                                       100.0%; Score 25; DB 2; 100.0%; Pred. No. 0.0098;
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                                                                                                                                                          Mismatches
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RESULT 9
US-09-023-655-1167/c
; Sequence 1167, Application US/09023655
; Patent No. 6607879
; Patent No. 6607879
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
ETLING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 619-792-8477
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Li, Lingna
APPLICANT: Lishko, Vali
TITLE OF INVENTION: MET
TITLE OF INVENTION: CO
NUMBER OF SEQUENCES: 3
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REFERENCE/DOCKET NUMBER: AN
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-792-3680
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Rel-Base #1.0, Version #1.25
CURRENT APPLICATION DATA:
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HYPOTHETICAL:
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LENGTH: 4646 base pair
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MEDIUM TYPE: Floppy disk
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                                                                                            APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OP INVENTION: COMPOSITION TITLE OP INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
                                                            CORRESPONDENCE ADDRESS:
                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Diego
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CITY: PALO ALTO
STATE: CALIFORNIA
                               STREET:
                                                ADDRESSEE:
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12526 High Bluff Drive, Suite 300
                              E: INCYTE PHARMACEUTICALS,
3174 PORTER DRIVE
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METHOD FOR DELIVERING BENEFICIAL COMPOSITIONS TO HAIR FOLLICLES
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                FOR
                                                                                                              THE DETECTION
                                                                                                                                                                                                                                                                                                                                                                         0.0099;
                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        Length 4646;
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US-09-023-655-1167
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
FILING DALE.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/332,444
APPLICATION SAME: 31-OCT-1994
                                                                                                                                                                                                                                              STREET: 6 L.
STREET: 8 L.
CITY: Roseland
CTATE: New Jersey
"TSA
                                                                                    SOFTWARE: DW4.V2
SOFTWARE: DW4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,276
FILING DATE: 05-JAN-1996
                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ent No.
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Carella,
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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IMMEDIATE SOURCE:
LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: ITLE OF INVENTION:
                                                                                                                                                           COMPUTER: IBM PS/2
OPERATING SYSTEM:
                                                                                                                                                                                                                                   COUNTRY: UZIP: 07068
                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 4646 base pairs
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5837536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            McDonagh, Kevin T
Nienhuis, Arthur
                                                                                                                                                                                                                                                                                                                        Carella, Byrne, Bain, Gilfillan,
Cecchi & Stewart
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                                                                                                                                                                                                inch diskette
                                                                                                                                                                                                                                                                                                                                                                                      IMPROVED EXPRESSION OF HUMAN
MULTIDRUG RESISTANCE GENES AND IMPROVED
SELECTION OF CELLS TRANSDUCED WITH SUCH
                                                                                                                                                              PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kevin T
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US-08-752-447-1
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US-08-752-447-1/c
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                                                                                                                                                                                                              TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/8 FILING DATE: 22-MAY-1992 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                             FEATURE:
                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: NO. 5994088nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
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                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 4669 bases
                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
             NAME/KEY:
LOCATION:
                                                                                                                                                                         STRANDEDNESS:
TOPOLOGY: lir
                                                            LOCATION:
                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 15-NOV-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: singular
                                                                                                         OCATION:
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                                                                                                                                                                                                                  4669 base pairs
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425..4264
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                             3'UTR
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              4265..4669
                                                                                                         1..424
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                                                                                                                                                                                                                                                                                                                                            Kevin E
                                                                                                                                                                                                                                                                                                               95,1121
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Pred. No. 0.0099;
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Query Match

100.0%;

Score 25;

DB 2;

Length 4669;

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RESULT 12
US-09-316-167-1/c
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/316,167
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
RESULT 13
US-09-397-233-1/c
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                                                                                                                                                                                             US-09-316-167-1
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                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-913-9808 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,44
FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: NO. 636357nan, Kevin E
NAME: NO. 636357nan, Sevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing
TITLE OF INVENTION: Using Immunoligcal Agents Specific
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                        LOCATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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STREET: Chicago
TTY: Chicago
Tllinos
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                                                                                                                                          Local
                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                          LOCATION:
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                                                                                                                                            Similarity
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                                                               AGCTTCCAACCACGTGTAAATCCTA 1041
                                                                                        AGCTTCCAACCACGTGTAAATCCTA 25
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425..4264
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1..424
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4265..4669
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                                                                                                                          100.0%; Score 25; DB 3; Length 4669; 100.0%; Pred. No. 0.0099; tive 0; Mismatches 0; Indels
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for P-glycoprotein
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LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-397-233-1
                                                                                                                                                                         RESULT 14
5206352-3/c
;Patent No. 5206352
; APPLICANT: Roninson, Igor B.;Pastan Ira H.;Gottesman,
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                                                                                                                                                                                                                                                                                                                                      ફ
                                                                                                                              ;Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA;SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
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Patent No. 6630327
GENERAL (INFORMATION:
APPLICANT: Mechetner, Eugene
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
                                                                                           NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                        APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-1999
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunological Agents Specific fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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1..424
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425..4264
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                                                                             US/07/622,836
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Pred. No. 0.0099;
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RESULT 15
5206352-3/c
;Patent NO. 5206352
; ARPLICANT: RONINBON, IGOT B.;Pastan Ira H.;Gottesman,
;Michael M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
;SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 992,575
; APPLICATION NUMBER: 982,575
; APPLICATION NUMBER: 845,610
; FILING DATE: 20-MAR-1986
; SEQ ID NO:3:
LENGTH: 4669
5206362-1
Search completed: Pebruary 9, 2005, 17:11:17 Job time: 79.592 secs
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FILING DATE: 28-MAR-1986
;SEQ ID NO:3:
LENGTH: 4669
                                                                                                                                                                        Query Match 100.0%; Score 25; DB 6; Length 4669; Best Local Similarity 100.0%; Pred. No. 0.0099; Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 25; DB 6; Length 4669; Best Local Similarity 100.0%; Pred. No. 0.0099; Matches 25; Conservative 0; Mismatches 0; Indels (
                                                                                       1065 AGCTTCCAACCACGTGTAAATCCTA 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AGCTTCCAACCACGTGTAAATCCTA 25
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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

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12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

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19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

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21: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Match Length DB	BB	ID	Description
. :	25	100.0	172	9	US-09-864-761-27462	Sequence 27462, A
0	25	100.0	209	15	US-10-101-510-284	Sequence 284, App
n u	25	100.0	219	9	US-09-864-761-27770	Sequence 27770, A
	25	100.0	463	ø	US-09-864-761-10820	Sequence 10820, A
0	25	100.0	. 473	9	US-09-864-761-11142	Sequence 11142, A
o e	25	100.0	2307	9	US-09-805-020-31	Sequence 31, Appl
0	25	100.0	3840	18	US-10-384-339C-30	Sequence 30, Appl
c E	25	100.0	3852	15	5 US-10-101-433A-1	Sequence 1, Appli
n	25	100.0	3860	9	9 US-09-866-866A-1	Sequence 1, Appli
c 10	25	100.0	3860	9	US-09-866-866A-3	Sequence 3, Appli
0 L	25	100.0	4186	17	17 US-10-619-359A-1	Sequence 1, Appli

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70.4 70.4 70.4 70.4	72.8 72.8 71.2	44.00		80.8 80.8	87.2 87.2	87.2 87.2	87.2 87.2	100.0	100.0	100.0	100.0	100.0	100.0	100.0
1792 50002 100554	325 22644 950	71251 44377 94720	4317 4369	2498 4317	4298 4788	4254 4254	4189 4254	8630 8630	4646 4669	4646 4646	4646 4646	4643	4643	4195 4533
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US-10-424-599-2071 US-10-424-599-26721 US-10-087-192-994 US-10-087-192-1165	-10-425-115-29 -10-087-192-44 -10-425-821-36	2-355 7-40 2-160	US-10-896-434-1 US-09-769-097-1 US-09-769-097-3	US-10-739-930-4420 US-10-044-671-1	7 3	US-10-388-934-265 US-10-152-319A-1484	-09-866-866A-	US-09-306-417-1 US-09-306-417-2	-775-169 -680-516	-10-641-643- -10-343-657-	-09-968-007A-74	-10-007-926A-	US-10-072-621-2 US-10-097-340-1	US-10-619-359A-3 US-09-805-020-30
Sequence 26721, A Sequence 994, App Sequence 1165, Ap	0 0 4 4 5 0	2 P P P P	Sequence 1, Appli Sequence 1, Appli Sequence 3, Appli	44	32, App]	<u>ي</u> ب ڊ		2	Sequence 198, Appli Sequence 1, Appli		74	258		Sequence 3, Appli Sequence 30, Appl

ALIGNMENTS

US-09-664-761-27462 US-09-664-761-27462 Sequence 27462, Application US/09864761 Patent No. US2002048765A1 APPLICANT: Pank, David R. APPLICANT: Penn, Sharron G. APPLICANTON NUMBER: US 60/180,312 PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-05-26 PRIOR FILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: US 60/207,456 PRIOR APPLICATION NUMBER: US 60/23,366 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US 60/236,359 PRIOR APPLICATION NUMBER: DET/US01/00666 PRIOR FILING DATE: 2001-01-30 PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR APPLICATION NUMBER: PCT/US01/00667 PRIOR APPLICATION NUMBER: PCT/US01/00669 PRIOR APPLICATION NUMBER: PCT/US01/00665
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ROBES USEFUL FOR
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APPLICATION NUMBER: PCT/US01/00668

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US-10-101-510-284
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                                                                               Query Match
Best Local Sin
Matches 25;
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SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 284
LENGTH: 209
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Matches
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APPLICANT: WAN, JACKSON
APPLICANT: WANG, YIXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 284, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local &
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                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE FILE REFERENCE: 15117.0012
CURRENT APPLICATION NUMBER: US/10/101,510
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/276,947
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: MAP TO AC005068.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64

OTHER INFORMATION: SWISSPROT HIT: P081873, EVALUE 3.00e-27

OTHER INFORMATION: NT HIT: AF016535.1, EVALUE 2.00e-92

OTHER INFORMATION: EST_HUMAN HIT: AW847648.1, EVALUE 2.30e+00
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                                                                                                                                                                                                            TYPE:
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ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21 APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-06-30
APPLICATION NUMBER: US 09/774,203
FILING DATE: 2001-01-29
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  204
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                                                                                                     Similarity
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AGCTTCCAACCACGTGTAAATCCTA 180
                                      AGCTTCCAACCACGTGTAAATCCTA 25
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                                                                             100.0%; Score 25; Di
llarity 100.0%; Pred. No. 0.(
Conservative 0; Mismatches
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                                                                                                   0.041;
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FEATURE:

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.71

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57

OTHER INFORMATION: NT HIT: M29428.1, EVALUE 1.00e-120

OTHER INFORMATION: SWISSPROT HIT: P08183, EVALUE 2.00e

US-09-864-761-27770
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Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron (
APPLICANT: Rank, David R
APPLICANT: "
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence
SEQ ID NO 27770
                                                              Matches
                                                                                     Query Match
Best Local :
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: "" ""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        ENGTH: 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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                                                                                     Similarity
AGCTTCCAACCACGTGTAAATCCTA 25
                                                         100.0%;
larity 100.0%;
Conservative 0
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1, David K.
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                                                         Score 25; DB 9;
Pred. No. 0.041;
; Mismatches
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                                                                                                         Length 219;
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                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                     OTHER INFORMATION: MAP TO AC005068.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.73
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.64
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CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Annomax Sequence Listing Engine vers. 
)EQ ID NO 10820
LENGTH: 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DR APPLICATION NUMBER: PCT/US01/00667
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00664
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00669
OR APPLICATION NUMBER: PCT/US01/00665
OR APPLICATION NUMBER: PCT/US01/00665
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00663
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00662
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APPLICATION NUMBER: PCT/US01/00666
FILING DATE: 2001-01-30
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APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
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APPLICATION NUMBER: US 60/234,687
FILING DATE: 2000-09-21
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APPLICATION NUMBER: PCT/US01/00661
FILING DATE: 2001-01-30
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     AGCTTCCAACCACGTGTAAATCCTA 364
                                             AGCTTCCAACCACGTGTAAATCCTA 25
                                                                                               100.0%; ilarity 100.0%; Conservative
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Pred. No. 0.
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RESULT 5
US-09-864-761-11142/c
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PRIOR APPLICATION UNMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR APPLICATION NUMBER: DCT/US01/00663

PRIOR APPLICATION NUMBER: DCT/US01/00663

PRIOR APPLICATION NUMBER: DCT/US01/00663
                                                                                                                                                                                               OTHER INFORMATION: MAP TO AC002457.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.42
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL :
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
US-09-864-761-11142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
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                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Chen, Wensheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                       LENGTH: 473
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                            FEATURE:
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                               AGCTTCCAACCACGTGTAAATCCTA 25
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Hanzel, David K.
                                                                                              100.0%; ilarity 100.0%; Conservative
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38: 49117
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                                                                                                                          Score 25;
Pred. No.
                                                                                                   Mismatches
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0.047;
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RESULT 8
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; PATENT DOCUMENT NUMBER: AF016535
US-10-384-339C-30
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CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR APPLICATION NUMBER: DE 1010586.5
PRIOR PILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-10-9
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 173
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US-10-384-339C-30/c
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US-09-805-020-31/c
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Publication No. US20020086384A1
GENERAL INFORMATION:
APPLICANT: LEVUNE, Zurit
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
CURRENT APPLICATION NUMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
                                                                                                                                          Matches
                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2307
TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1)..(2307)
OTHER INFORMATION: any n = a,c,g,t any unknown
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                                                        AGCTTCCAACCACGTGTAAATCCTA 617
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100.0%; Pred. No. 0.
ative 0; Mismatcher
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US-09-866-866A-3/c
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; TYPE: DNA; Homo sapiens US-09-866-866A-1
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                                                                                Query Match
                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/584/586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hanscom, Sara
APPLICANT: Crespi, Charles
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307/70019
CURRENT APPLICATION NUMBER: US/10/101,433A
CURRENT FILING DATE: 2002-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sorrentino, Brian APPLICANT: Schuetz, John
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PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 38
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LOCATION: (1)..(3852)
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                                                                                                                                                                                                                      LENGTH: 3860
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641 AGCTTCCAACCACGTGTAAATCCTA 617
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                                                                                               100.0%; Score 25; DB 9; 100.0%; Pred. No. 0.068;
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100.0%; Pred. No. 0.068;
tive 0; Mismatches
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GENERAL INFORMATION

APPLICANT: Sorrentino, Br. APPLICANT: Schuetz, John

Brian

Sequence 3, Application US/09866866A Patent No. US20020102244A1

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RESULT 12
US-10-619-359A-3/c
US-10-619-359A-3/c

1 Sequence 3, Application US/10619359A
1 Publication No. US20040077000A1
1 Publication No. TON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILLE REFERENCE: G00307.70020. US
CURRENT APPLICATION NUMBER: US/10/619,359A
CURRENT FILING DATE: 2003-07-14
PRIOR PELLANTION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR APPLICATION NUMBER: US 60/158,810
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 1999-10-12
PRIOR FILING DATE: 2000-09-28
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CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-38
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 18 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, I
APPLICANT: CRESPI, CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 3860
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4186
TYPE: DNA
ORGANISM: Macaca fascicularis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: (100)...(3940)
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STOCKER, PENNY J.
STEIMEL-CRESPI, DOROTHY T.
CRESPI, CHARLES L.
                                                                                                                                                                                                                             AGCTTCCAACCACGTGTAAATCCTA 716
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ilarity 100.0%;
Conservative 0
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Pred. No. 0.069;
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Query Match
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Matches 25; Conserve
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                                                                                                                                                                                                   RESULT 14
US-10-072-621-2/c
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CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: LEVINE, Zurit
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09805020 Publication No. US20020086384A1
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                         Sequence 2, Application US/10072621 Publication No. US20020169137A1
                                                                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT FILING DATE: 2003-07-14
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/158,818 PRIOR FILING DATE: 1999-10-12 PRIOR APPLICATION NUMBER: US 09/672,810
                           APPLICANT: Reiner, Peter B.
APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
THE PROPERSOR : ACCIO A MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Macaca fascicularis FEATURE:
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LOCATION: (100)...(3949)
CURRENT APPLICATION NUMBER: US/10/072,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature LOCATION: (1)...(4533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4195
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Pred. No:
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APPLICANT: ROSEMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GLATT
ITILE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
ITILE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-072-621-2
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                                                                                                                                                   Best Loc
Matches
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APPLICANT: Manjula GANNA
APPLICANT: Sebastian HOE
APPLICANT: Shubhangi KAM
APPLICANT: Steve G. KOVA
APPLICANT: Rachel E. MEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 25; DB 13; Length 4643; Best Local Similarity 100.0%; Pred. No. 0.07; Matches 25; Conservative 0; Mismatches 0; Indels 0
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NUMBER OF SEQ ID NOS: 10
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 2
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                                                                                                                                            / Match 100.0%; Score 25; DB 14; Length 4643; Local Similarity 100.0%; Pred. No. 0.07; Indels 0 25; Conservative 0; Mismatches 0; Indels 0
   1065 AGCTTCCAACCACGTGTAAATCCTA 1041
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Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gordon B. MILLS
Robert C. BAST, Jr.
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Search completed: February 9, 2005, 22:26:39 Job time: 267.667 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	PAKOKISS	AAK32026	ABS06048	ABS30977	AAK05682	AAK31296	AAI37193	ABS19335	AAK19129	AAK45086	ABZ35172	ABS18622	ABS44044	AAK18477	AAK44387	AAI50383	ABK87743	ABK87742	AAD39001	AAD39011	ID
	Aak06359 Human bra	Aak32026 Human bon		Abs30977 Human liv	Human	Human	Probe	Human	Aak19129 Human bra	Human	Human	Abs18622 Human gen	Abs44044 Human liv	Aak18477 Human bra	7 Human	Probe	Multip	•	Aad39001 Human mdr	Human	Description

26-OCT-2000; 2000US-0243542P.

(BGHM) BRIGHAM & WOMENS HOSPITAL INC.

25-OCT-2001; 2001WO-US049856

02-MAY-2002. WO200234291-A2

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1 binding molecules.

WPI; 2002-471427/50.

Colgan SP;

C 45	C 44	~	c 42	C 41	C 40	c 39	ω	c 37	c 36	c 35	c 34	c 33	c 32	c 31	c 30		ผ	N	c 26	ผ		c 23		C 21	2
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ABX77217	ABV74349	ABV94267	ABS76368	ABS65229	AAQ04522	AAH57442	AAV66534	AAV66533	AAF86128	AAF86127	AAZ88973	ABA94366	ABA94365	AAZ49333	AAZ49332	ABT14496	ABQ78185	ABL91687	ABX09965	ABZ35722	ABV78146	ABS65230	AAN70751	ADOOD / CA	ABS06792
Abx77217 cDNA enco	Abv74349 Human ABC				MULC							Human	Human	Human	Human	Kileso		Human	Human	Human			•		Abs06792 Human gen

ALIGNMENTS

Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphotid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; ds. AAD39011; AAD39011 standard; DNA; 25 Human mdrl gene HIF-1 binding site DNA #4. 23-SEP-2002 (first entry) misc_binding Homo sapiens. Location/Qualifiers
11. .15
/*tag= a /bound_moiety= "HIF-1" ₽₽

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Best Local
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          Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMO-1 binding molecules or antisense molecules are useful for treating a subject having or at risk of developing haematologic malignancy or MDR (e.g. a lymphoid disorder or a myeloid disorder. The lymphoid disorders include lymphocytic leukaemia or chronic lymphoproliferative disorders e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia, e.g. angiogenic myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The invention is used in gene therapy. The present sequence is human mdrl
                                                                             WPI; 2002-471427/50
                                                                                                                                                                           26-OCT-2000; 2000US-0243542P
                                                                                                                                                                                                         25-OCT-2001; 2001WO-US049856
                                                                                                                                                                                                                                                                                                                                                                         Key
                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                           (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                      modified_base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive (HRE) binding molecules or antisense nucleic acid molecules and
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/mod_base= OTHER
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Pred. No. 0.025;
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   The invention relates to a primer for amplifying a nucleic acid comprising a 15 to 30 base continuous oligonucleotides of an MDR1 (multiple drug resistance gene 1) gene fragment appearing as ABK87740. Also included are a kit for quantitatively determining the expression level of MDR1 gene, a probe for capturing a nucleic acid, a reagent fo amplifying a nucleic acid and diagnosis of the drug resistance of a patient. The primer is useful for the determination of MDR expression level by nucleic acid amplification. The present sequence is a fragmen
                                                                                                                                                                                                                                                                                                                                                                       A primer for amplifying a nucleic acid comprises a specific oligonucleotide sequence for determination of Multiple Drug gene expression level by nucleic acid amplification.
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                          AAI50383;
                                                                           AAI50383 standard; DNA; 172 BP
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25; Conserv
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                                                                                                                                                                                                                                                       AGCTTCCAACCACGTGTAAATCCTA 25
                                                                                                                                                                                                     AGCTTCCAACCACGTGTAAATCCTA 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               즛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                        21 G; 28 T; 0 U; 0
                                                                                                                                                                                                                                                                                                                               Score 25; DB 6
Pred. No. 0.03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MDR1, sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                       Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                           Other;
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RRESULT 6
AAK44387
ID AAK4
XX AAK4
XX AAK4
XX AAK4
XX Huma
XX Huma
XX Huma
XX Homc
XX Hom
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-2001
                                                                                                                                                                                                                                  Human; bone microarray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200157272-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488897/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-2000; 2000US-0180312P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human
                                                                                                                                                                                                                                                                                                       Human bone marrow expressed single exon probe SEQ ID NO: 18944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MOLE-)
04-FEB-2000; 2000US-0180312P
                                              30-JAN-2001;
                                                                                             09-AUG-2001
                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                          06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAK44387 standard; DNA;
                                                                                                                                            WO200157276-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome-derived single exon nucleic acid probes useful for analyzing expression in human placenta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   microarray; human; placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%;
1 Similarity 100.0%;
25; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    172 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTTCCAACCACGTGTAAATCCTA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 19069; 654pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanzel
                                                                                                                                                                                                                                       cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                 2001WO-US000668.
                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 A; 43 C; 29 G; 42 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            expressed exon;
; leukaemia; lym;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          172
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank DR,
                                                                                                                                                                                                                                         lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                         gene expression analysis; probe; phoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antenatal diagnosis;
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0.032;
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RESULT 7
AAK18477
ID AAK1
XX AAK1
AC AAK1
XX O5-N
XX Huma
XX Huma
XX Huma
XX Homc
XX Hom
XX Ho
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            samples, which may enable the such as lymphoma, leukaemia the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK18477 standard; DNA; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 172 BP; 58 A; 43 C; 29 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
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                                                                                                                                                                                                                       (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon nucleic sxpression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which are derived from genomic sequences arrow. They can be used to measure gene ex
                                                                                                                                                                                                                       MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTCCAACCACGTGTAAATCCTA 86
                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel
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                                                                                                                                                                                                                                                                           2000US-00632366.
2000US-0234687P.
2000US-0236359P.
2000US-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n expressed exon; gene expression analysis; probe; microarray; disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention provides a number of single exon
                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0180312P.
2000US-0207456P.
2000US-00608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      leukaemia and myeloma. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               can be used to measure gene expression in borenable the improved diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                                                                                                                                                       Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single exon
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Pred. No.
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Matches 25
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26-MAY-2000;
30-JUN-2000;
The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-2000;
21-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; nurrofibromatosis; caucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; Hermansky-pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary cillary dyskinesis; pulmonary hypertension; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                associated with coronary heart disease. ABS25011-ABS51005 represent liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genome-derived single exon probe ORF from lung SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                           Claim 4;
                                                                                                                                                                                                                                                                                                                                                                Spatially-addressable set of single exon nucleic measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN<sup>-</sup>2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGCTTCCAACCACGTGTAAATCCTA 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTTCCAACCACGTGTAAATCCTA 86
                                                                                                                                                                                                                                                                                                           SEQ ID NO 18613; 634pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease; open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 43 C; 29 G; 42 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame; ORF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.032;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  acid probes, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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cc collection of detectably labeled nucleic acids derived from human lung cc mRNA, and (b) measuring the label detectably bound to each probe of the clarray; identifying exons in a eukaryotic genome, comprising (a) collections at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably cc having a fragment identical to the predicted exon, to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several ct issues and/or cell types using hybridisation to a single exon of the exons should be assigned to a single gene, a common pattern of the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the compression of the exons and for identifying exons in a gene, particularly using human claratery chronic obstructive pulmonary disease (COPD), interstitial lung cancer, sarcoidosis, pulmonary haemosiderosis, neurofibromatosis, chief the sarcoidosis, pulmonary haemosiderosis, neurofibromatosis, chief the sarcoidosis, pulmonary haemosiderosis, pulmonary collary colla
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ABZ35172/c
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 172 BP; 58 A; 43 C; 29 G; 42 T;
                                                                                                                                                                                                                                                                                                                                                                               bronchial epithelium; prostate; muscle; lung fil
tumour; microarray; genome mapping; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene expression profile polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABZ35172 standard;
                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2003
                                                                                                                                                          20-MAR-2001; 2001US-0276947P
                                                                                                                                                                                                    20-MAR-2002; 2002WO-US008456
                                                                                                                                                                                                                                                                                    WO200274979-A2
                                                                                                                      (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC
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                                                                                                                                                                                                                                                                                                                                                                expression;
                                                                                                                                                                                                                                                                                                                                                                                      artery; endothelium; umbilical; vein; aorta; pulmonary artery;
ial epithelium; prostate; muscle; lung fibroblast; osteoblast;
; microarray; genome mapping; antibiotic; antiviral; antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 172;
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                                                                                                                                                                                                                                                                                                                                                                                            antifungal;
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New gene expression profile generated from primary, endothelial.

WPI; 2002-740862/80

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RESULT 11
AAK45086/c
ID AAK450
XX AAK450
XX AAK450
XX Human;
KW Human;
KW microa
XX Homo B
XX HO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a gene expression profile comprising one or more C genes (ABZ31889-ABZ35892) and generated from a cell type. The cell type is a coronary artery endothelium, umbilical artery or vein endothelium, coronary artery c endothelium, myometrium microvascular endothelium, pulmonary artery c epithelium, bronchial epithelium, renal epithelium, renal proximal tubule epithelium, seral cortical epithelium, renal proximal tubule epithelium, small airway epithelium, renal epithelium, umbilical artery smooth seral fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes, c dermal fibroblast, neural progenitor muscle, lung fibroblast, c determining the coronary artery smooth muscle, set collaborate stromal cell. The gene expression profile is used c for determining the level of RNA expression for a sample, determining the capression profile is used in the separation profile may provide meaningful information with respect to tumour type and stage, treatment methods, and prognosis. The gene or protein expression profile may also be used for creating microarrays. The microarray is useful for medical diagnosis, genotyping of organisms, confirming cell or tissue identifications and in identifying promising antibiotics, antiviral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FFX@XDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
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Best Local S
Matches 25
                                                                                                                                                                                                                                         04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray;
                                                                                                                                                                                                                  03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; bone marrow expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-NOV-2001
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                                                                         (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bone
                                                                         MOLECULAR
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
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2000US-0234359P.
2000US-0234359P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP;
                                                                                                                                                                                                                                                                                                                                                             2001WO-US000668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                 DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
                                                                         DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                 Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ç
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     xon; gene expression analysis; probe;
lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                 DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Η,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
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RESULT 12
AAK19129/c
ID AAK191
XX AAK191
XX AAK191
XX DT 05-NOV
DE Human;
KW Human;
KW Alzhei
KW SB.
XX WO2001
XX WO2001
XX O4-FEE
PR 26-MAY
PR 30-JUN
PR 03-AUG
PF 30-JUN
PR 04-FEE
PR 27-SEF
PR 26-MAY
PR 30-JUN
XX PR 10-SEF
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PR 28-MAY
PR 30-JUN
XX TABE
PR 27-SEF
PR 27-SEF
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PR
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-02346359.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                               Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAK19129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAK19129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 219 BP; 54 A; 38 C;
                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-488900/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome-derived single exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brain expressed exon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ب
                                                                                                                                                                                                                                                                                                                                                                     MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; SEQ ID NO 19643; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTTCCAACCACGTGTAAATCCTA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCTTCCAACCACGTGTAAATCCTA 119
                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                        Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ed exon; gene expression analysis; probe; microarray;
multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    provides a number of single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 BP
                                                                                                                                                                                                                               probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone marrow
                                                                                                                                                                                                                                                                                                                        Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                            for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No.
                                                                                                                                                                                                                                                                                                                        DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID NO: 19120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                 human
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The present invention proved from genomic sequences expressed in the numerical probes which are derived from genomic sequences expressed in the numerical brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

present invention provides a number of single exon nucleic acid

Example

4.

SEQ

ID NO

19120;

650pp +

Sequence

Listing;

English

expression

ä

exon

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RESULT 13
ABS19335/c
ID ABS19335/c
XX ABS193
XX ABS193
XX 19-AUG
XX Human;
KW Chroni
KW Chroni
KW Chroni
KW Priman;
KW Priman
XX Human;
KW Human;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiccytosis; lymphangioletomycmtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension; hyaline membrane disease; open reading frame; ORF.
                        The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes in the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mann, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a sukaryotic genome, comprising (a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; ds; single exon probe; asthma; lung cancer; COPD; ILD chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US000665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-NOV-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; SEQ ID NO 19326; 634pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2000;
      algorithmically predicting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genome-derived single exon probe ORF from lung SEQ ID No 19326.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AGCTTCCAACCACGTGTAAATCCTA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTTCCAACCACGTGTAAATCCTA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 4;
100.0%; Pred. No. 0.033;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ü
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 G;
         least one exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lung samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
      from genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease;
      sequences
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RESULT 14
AAI37193
ID AAI377
XX AAI37
XX AAI37
XX Probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC tissues and/or cell types using hybridisation to a single exon committee and/or cell types with the exon, where a common pattern of the expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one compression of the exons should be assigned to a single gene; a peptide comprising one compression of 12011 sequences, mentioned in the specification, or encoded by the compression of the probes are used for gene expression canalysis, and for identifying exons in a gene, particularly using human canalysis, and for the study of lung diseases such as aschma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung cancer, chronic obstructive pulmonary disease, such as aschma, lung consess (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, cuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-compadiate syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary colliary compadiates, lumonary haemosiderosis, pulmonary colliary compadiates, pulmonary spote open reading frame of the compadiate of the printed specification, but was obtained in electronic format directly cancer in the printed specification, but was obtained in electronic format directly cancer in the compadiate of the printed specification, but was obtained in electronic format directly cancer.
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Best Local
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26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                             03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe #5879 used to measure gene expression in human placenta sample
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                                                                                                                                                                                                             MOLECULAR DYNAMICS INC
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                                                                                                                                      Hanzel
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                                                                                                                                                                                                                                                                                                                                             2000US-00608408.
2000US-00632366.
2000US-0234687P.
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                                                                                                                                      Chen W,
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Pred.
                                                                                                                                          Rank DR
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Human genome-derived single exon nucleic acid probes useful for analyzing

WPI; 2001-488897/53.

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RESULT 15
ARX31296
ID ARX31296
ID ARX31
AC AAX31
AC AAX31
AC AAX31
AC AAX31
AX Human
XX Human
XX Homo
DX Homo
DY Homo
DY JA-EE
PR 26-MA
DR 30-JU
PR 27-SE
PR 27-SE
PR 27-SE
PR 27-SE
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PR 27-SE
PR 103-AU
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PR 103-AU
PR 27-SE
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PR 27-SE
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   Query Match
Best Local S
Matches 25
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Best Local Similarity
Matches 25; Conserv
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                              probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancer such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                           Sequence 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
                                                                                                                                                                                                                                                                                                                                   The present invention provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                         Example 4; SEQ ID NO 5853; 658pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-488900/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene expression in human placenta.
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ch 100.0%; Score 25; DB 4; 1 Similarity 100.0%; Pred. No. 0.036; 25; Conservative 0; Mismatches 0;
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                                                                                                                              BP; 153
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                                                                                                                     A; 100 C; 98 G; 112 T; 0 U; 0 Other;
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                                                         DB 4; Length 463;
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Gaps
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Search completed: February 9, 2005, 16:05:58 Job time : 247.69 secs

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Title:
Perfect score:
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 857: 4
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 Query
Match
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Copyright (c) 1993 - 2005 Compugen Ltd.
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gb_est3: *
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gb_est5: *
gb_est6: *
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AX0303956
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BH174634
BH713924
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BI691631 60307314
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BH713924 BOMC187TF
BH696214 BOMC167TF
AZ341385 FM00773B15
CC951154 BOIGM45TF
BH98332 odf02c02.
BZ010051 oej74097.
CC967311 BOIHM63TR
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AI965324	BH858849	BH858848	BF808478	BF805641	BF806551	BB872680	BI301966	BI301745	CR055056	AZ001999	CR063094	CE015031	AK086811	AG425665	AK090183	BZ501403	009091	BZ493588	BH068818	111000110
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ALIGNMENTS

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Qy	Query Mat Best Loca Matches	gene ORIGIN	COMMENT FEATURES Source	REFERENCE AUTHORS TITLE JOURNAL	AUTHORS AUTHORS TITLE JOURNAL PUBMED	RESULT 1 AV408954/c LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
1 AGCTTCCAACCACGTGTAAATCCTA 25	Query Match 100.0%; Score 25; DB 9; Length 3843; Best Local Similarity 100.0%; Pred. No. 0.28; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/mol type="genomic DNA" /db xref="taxon:9606" <13843 /gene="ABCB1" /locus_tag="HCM3396"		<pre>2 (bases 1 to 3843) 2 (bases 1 to 3843) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M. Direct Submission Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA</pre>	40.00000	AY408954 3843 bp DNA linear GSS 15-DEC-2003 Homo sapiens ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence, AY408954 AY408954.1 GI:39764922 GSS. Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

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                                                                                                                                                                                                                                                                                                                                                                      3182 bp mRNA linear HTC 03-APR-20 Mus musculus 11 days pregnant adult female ovary and uterus cDNA, RIKEN full-length enriched library, clone:5031438E12 product:ATP-binding cassette, sub-family B (MDR/TAP), member 1B. full insert sequence.
                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                   Mus musculus
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Mus musculus (house mouse)
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This sequence was made by sequencing geno
                                                                                                                                                                                                                                                                                                                       AK030328.1 GI:26081769
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Mammalia; Eutheria; Primates;
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/db_xref="taxon:9598"
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/locus_tag="HCM3396"
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18 (bases 1 to 3182)

28 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Fukuda, S., Furuno, M., Hanagaki, T., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Salto, R., Saito, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tagawa, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokoha Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URLihttp://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
Division of Experimental Animal Research in Riken contribu
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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                                                                                                                                                                                                                                                                                                                                      URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                Please visit our web site for further details.
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/tissue_type="ovary and uterus"
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/dev_stage="ll days pregnant adult"
                                                                                                                 clone="5031438E12"
                                                                                                                                              /db_xref="FANTOM_DB:5031438E12"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                       organism="Mus musculus"
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Euteleostomi; Sus.

with

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Sus scrofa (pig)
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3816)

Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence was made by sequencing genomic exons and ordering
based on alignment.
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1. ..>3816
                                                                                                                                                                                                                                                                                                             'gene="ABCB1"
'locus_tag="HCM3396"
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Pred. No. 11;
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Best Local Similarity 91.7%;
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Single pass sequencing. Bases called with
trimmed with the aid of the trim_alt optic
cross match v0.990329.
Plate: SRG8002 row: F column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2003)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i (bases 1 to 682)
Smith, T.P.L., Freking, B.A., Ford, J.J., Vallet, J.L., Fox, J., Smith, T.P.L., Nonneman, D.J., Wray, J.E. and Keele, J.W.
A second set of porcine BSTs from a pooled-tissue normalized
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Fax: 402 762 4390
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Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                        BE217416
fbn-i094 Cattle pUC18 Library
BE217416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                      Tel: 0049-038208-68700
Fax: 0049-038208-68702
Email: schwerin@fbn-dummerstorf.de
                                                                                                                                                                                                                                                                       1 (bases 1 to 478)
Schwerin, M., Dorroc
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Mammalia; Eutheria;
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2nd Wilhelm-Stahl-Allee,
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Contact: Schwerin M
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                                                                     POLYA=Yes.
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/lab host="DH10B"
/lab host="DH10B"
/clone lib="MARC 3PIG"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
/instary made with RNA pooled from multiple tissues
including brain, liver, muscle, placenta/endometrium,
ovary, testes, and bone marrow."
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/mol_type="mRNA"

/db_xref="taxon:9823"
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 /organism="Bos taurus"
/mol_type="mRNA"
                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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                                                                                                                                                                                                                                                                                                                                                           AL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V. Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,
Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,
Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-Length' CDNA Sequences:
A Combined Approach to Evaluate and Improve Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; cosida; eurosida; II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSOA1N4 806 bp mRNA linear HTC 06-FEB-200 Arabidopsis thaliana Full-length cDNA-Complete sequence from clone GSLTSIL25ZG04 of Silique of strain col-0 of Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                   http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX832952.1 GI:42459179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCTTCCAACCTTCTGTAAATCCTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTTCCAACCACGTGTAAATCCTA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 806)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                 /gene="At5g51440"
                                                                                                             /plasmid="pCMVSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Intestine"
/dev stage="lactation"
/lab_host="X11-blue"
/clone_lib="Cattle pUC18 Library"
/note="Vector: pUC18 Sma I/BAP"
                                                                                                                                        /clone="GSLTSIL25ZG04"
/tissue_type="Silique"
                                                                                                                                                                                      db_xref="taxon:3702"
                                                                                                                                                                                                              strain="Col-0"
                                                                                                                                                                                                                                                        organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                     . 806
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                                                                                                                                                                                                                                  type="mRNA"
80.8%;
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Score 20.2;
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Pred. No. 5
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Length 806;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ957679
AZ957679.1 GI:13828906
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 0224 row: F column: 07
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ957679
489 bp DNA linear GSS 2: 2M0224F07R Mouse 10kb plasmid UUGC2M library Mus musculus clone UUGC2M0224F07 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0224 row: F column: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTTCCAACCACGTCTAAATCCAA 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                             10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pDD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and
                      purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                     polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through (0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 was blunt end-repaired with T4 DNA polymerase and T4
                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                             Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: FWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lone="UUGC2M0224F07"
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0; Mismatches
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ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                   (female) was obtained from the Jackson
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Query Match

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Score 19.8;

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RESULT 9
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Best Local &
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603307314F1 NCI_CGAP_Mam6 Mus
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CDNA Library Preparation: Life Technogies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                       BH521842
BH521842.1 GI:17729927
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
Brassica oleracea
Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                              BOGQF60TF BOGQ Brassica oleracea genomic clone BOGQF60,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plate: LLAM11872 row: k column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                     BH521842
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                                                                                                                                                                                                                                                                                   AGCTTCCAACCACGTGTAAATCC 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mmalia; Eutheria; (bases 1 to 775)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            quality sequence stop:
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:5343483"
/sex="female, virgin"
/tissue type="infiltrating d'
/dev_stage="5 months"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Mam6"
                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sall; Site 2: NotI; Cloned unidirectionally. Primer: Ōligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mol_type="mRNA
strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:15654260
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91.3%;
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                                                                                                                                                                                                                                                                                                                                          Score 19.8;
Pred. No. 90;
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musculus cDNA clone IMAGE:5343483 5',
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AUTHORS
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VERSION
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AU291400
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Best Local
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                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                     Zinnia elegans
Zinnia elegans
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Zinnia.
1 (bases 1 to 553)
1 (bases 1 to 553)
Horiquchi,G., Kishimoto,N., Kubo,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 526)
1 Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Francoun, C.D., Van Aken, Brancoung of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _
                                                                                                                                                                                         Visualization by comprehensive microarray analysis of gene expression programs during transdifferentiation of mesophyll cells into xylem cells. Sci. U.S.A. 99 (24), 15794-15799 (2002) Contact: Taku Demura Morphogenesis Research Group RIKEN Plant Science Center 1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehirocho, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU291400 zinnia cultured mesophyll cell equalized elegans cDNA clone Z6035, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole genome shotgun sequencing Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                            Demura,T., Tashiro,G., Horiguchi,G., Kishimoto,N., Kubo,M., Matsuoka,N., Minami,A., Nagata-Hiwatashi,M., Nakamura,K., Okamura,Y., Sassa,N., Suzuki,S., Yazaki,J., Kikuchi,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                    Fukuda, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zinnia elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU291400.1 GI:24251908
                                                                                              Email: demura@postman.riken.go.
This clone was obtained at our
Seq primer: M13 forward.
                                                                                                                                                             Fax: 81-45-503-9573
                                                                                                                                                                             Tel: 81-45-503-9605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="BOGQ"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="TO1000DH3"
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       /organism="Zinnia elegans"
/mol_type="mRNA"
/cultivar="Canary bird"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="BOGQF60"
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87.5%;
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Pred. No. 1.7e+02;
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laboratory
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Length 526; Indels

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EST 04-DEC-2002 cDNA Zinnia

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RESULT 13
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Schalkwyk,L.C., Cusack,B., Dunkel,I., Hopp,M., Kramer,M., Palczewski,S., Piefke,J., Scheel,S., Weiher,M., Wenske,G., Lehrach,H. and Himmelbauer,H.
Advanced integrated mouse YAC map including BAC framework Genome Res. 11 (12), 2142-2150 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Vertebrate Genomics/ Abtlg. Lehrach
Max-Planck-Institute of molecular Genetics
Ihnestr.73, D-14195 Berlin-Dahlem, Germany
Email: himmelbauer@molgen.mpg.de
Information on marker localization (Chromosome, map segment) and
YACs positive for this probe can be obtained from our web site
http://www.molgen.mpg.de/(tilde)rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bir51B20 Mouse IRS-PCR fragment
genomic clone Bir51B20, genomic
BH174634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                               AGCTTACAACCACCTGTAACTCCT
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nilarity 87.5%;
Conservative
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llarity 87.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B1-PCR
                                                                                                                                                                                                                                                                         /lab_host="E.coli DH5alpha"
/clone lib="Mouse IRS-PCR fragment library 57R/bir"
/note="Vector: pAMP10 (Gibco-BRL); The library was
generated from IRS-PCR fragments obtained by amplification
of genomic mouse DNA with the mouse B1-repeat primer B1R
(5'-AGTTCCAGGACAGCCTAYACAGA-3'). Additional
                                                                                                                                                                                                                                        information online at
www.molgen.mpg.de/~rodent/html/introduction.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="mesophyll cell"
/clone Tib="zinnia cultured mesophyll cell equalized cDNA"
/note="Vector: pGEM-T eass; cultured in tracheary element
differentiation-inductive medium"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/strain="C57BL/6"
                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="Bir51B20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
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                                                                                                                                         Score 19.2; DB 8;
Pred. No. 1.7e+02;
0; Mismatches 3;
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Pred. No. 1.7e+02;
0; Mismatches 3;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rossids; eurosids I; Brassicales; Brassicaceae; Brassica.
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                                                    9712 Medical Center Drive,
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                           1 (bases 1 to 617)
Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
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BOMNB04TR BO_2_3_KB Brassica oleracea genomic clone BOMNB04.
                                                                                                                                          Other_GSSs: BOMNBO4TF
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BH713924
BH713924.1 GI:18806913
                Email: cdtown@tigr.org
DNA is from a doubled haploid
                                                                                                                             Contact: Chris Town
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Fax: 301-838-0208
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Unpublished (2001)
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BOMCI38TF BO_2_3_KB Brassica
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DNA is from a doubled haploid provided by
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primer: TR
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
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/mol_type="genomic DNA"
/strain="Tol000DH3"
/db_xref="taxon:3712"
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87.5%;
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Pred. No. 1.
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                  provided by Tom Osborn
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Best Local Similarity 87.5%;
Matches 21; Conservative
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1 (bases 1 to 634)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)

Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH698731 634 bp DNA linear GSS 20-F BOMCI67TF BO_2_3_KB Brassica oleracea genomic clone BOMCI67, genomic survey sequence.
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Brassica oleracea
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Class: sheared ends.
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                                                                                                                                                                                                            /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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                                                                                                                               76.8%; Score 19.2; DB 8;
87.5%; Pred. No. 1.7e+02;
tive 0; Mismatches 3;
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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GenEmbl:*
1: gb ba:*
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4553	4378	4264	4264	4192	3988	3988	3988	3860	3860	3843	3840	3489	768	765	765	765	25	25	Length
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AX706975 AX707905	AR028672	AX012321	AX012320	AR306492	AR306491	AR028671	AR405961	AR363344		•	AR091275 Sequence	AR055785	M14758 Homo sapien	AX504298	AX391099	AX336708			149610 Sequence	CQ861565			AX522070	CQ815440
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ALIGNMENTS

RESULT 2 AX504327/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy dd	Query Match Best Local Matches 2	ORIGIN	FEATURES	JOURNAL	REFERENCE AUTHORS TITLE	KEYWORDS SOURCE ORGANISM	RESULT 1 AX504310 LOCUS DEFINITION ACCESSION VERSION
AX504327 Sequence 30 from Patent WO0234291. AX504327 AX504327.1 GI:23386139 Homo sapiens (human)	1 GTGACATTTTCACGGCCATAGCGAA 25 	/ Match 100.0%; Score 25; DB 6; Length 25; Local Similarity 100.0%; Pred. No. 0.14; nes 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"		multiple drug resistance Patent: WO 0234291-A 13 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)	1 Colgan,S.P. Compositions and methods for treating hematologic malignancies and	Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX504310 25 bp DNA linear PAT 27-SEP-2002 Sequence 13 from Patent WO0234291. AX504310 AX504310.1 GI:23386128

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  Heinrich,G. and Kerb,R. Methods for treatment of cancer using Patent: WO 03013536-A 674 20-FEB-2003; Epidauros Biotechnologie AG (DE) Location/Qualifiers
                                                                                                                                                     Eukaryota;
                                                                                                                                                                                                                                                          AX707906
Seguence 674 from Patent
AX707906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
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Patent: WO 0234291-A 30 02-WAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC.
Location/Qualifiers
                                                                                                                                                                         Homo
                                                                                                                                                                                          Homo sapiens (human)
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Methods for the treatment of cancer with
Patent: WO 03013534-A 674 20-FEB-2003;
Epidauros Biotechnologie AG (DE)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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llarity 100.0%;
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoproteins
J. Biol. Chem. 265 (1), 506-514 (1990)
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1 (bases 280 to 437)
Chin,J.E., Soffir,R., Noonan,K.E., Choi,K. and Roninson,I.B.
Chin,J.E., Soffir,R., Thousan, M.B. (P-glycoprotein) gene
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Chen, C.J., Clark, D.
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M29432.1 GI:187481
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/gene="PGY1"
/note="PGY1,
536. .739
                                                                               /gene="PGY1"
/note="P-glycoprotein"
/number=12
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Homo Bapiens P-glycoprotein (
AY490254
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Direct Submission
Submitted (30-NOV-2003) Human Molecular
Submitted P.O.,
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AB029153
Felis catus multi-drug
AB029153
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                                                                                                GTGACATTTTCACGGCCATAGCGAA 651
                                                                                                               GTGACATTTTCACGGCCATAGCGAA 25
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/note="P-glycoprotein"
/number=13
                                                                                                                                                                                                                                  /codon_start=1
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/protein id="AAR99172.1"
/db_xref="GI:41058415"
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KVQSSQTVALYGNSGGKSTTVQLMQRLYDFTEGMLEFQLQMYESHTYFLFQVSVDGQ
DIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGRENVTMDEIEKAVKEANAYDFIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PGY1"
/note="PGY1, intron
                                                                                                                                                                                                                                                                                                                                                          /product="P-glycoprotein"
join(<16. .126,297. .422,
                                                                                                                                                                                                                                                                                                                                  /gene="MDR1"
/note="transporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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gene="MDR1"
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100.0%; Pred. No. 0.:
tive 0; Mismatches
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              3489 bp
resistance
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AX481416/c
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Matches 25; Conserv
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Tsujimoto, H. and Okai, Y.
Direct Submission
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Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
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NKNLEEAKRIGIKKAITANISIGIRELLIYASYALAPWGTGLVLSHEYSIGOVLTVF
FSVLLGAFSVGQASPSIEAFANARGAAYEIFKIIDNKPSIDSYSKKYGHKEDNIKGNLE
FKNYHESYPSRKEVEKLIKGALHKVOSGOVVALVGNSGCGKSTTVQLMQRIYDPTDGMV
SIDGODIRTINVRYLREIIGVVSQEPVLFATTIAEBURYGRENVTMEEIEKAVKEANA
YDETNKLPNKEDTLVGERGAQLSGGOKQRIAAAALVRENKILLLDEATSALDSESEA
VVQVALDKAKKGRTTIVVAHKLSTIRNADVLAGFDDGVIVEKGNHDELMKEEGIYFKL
VTMQTRGNEIELENAVYESISEIDALEMSPKDSGSSLIRRRSTRKSHHASQGORKALG
TKENLDERVEPVSFWRILKLMITEMPYFVVGJFCAIINGCLQPAFSVILSRIIGVFTR
VEDDETKRQNSNIRSLLFLYLGIISSITFFLQGTFGKAGEILTKRLEYMVFRSMLRQ
DVSWFDDPKNTTGALTTRLANDAAQVKGAIGSRLAIITONIANLGTGIIISLIYGWQL
TLLLLAIVPIIA IGGVESMKYLSGQALKDKKELEGAGKVATEAIENFRTVVSLTREQK
FEYMYAGSLOVPYNSLIRKAHIFGISFSITQAMMYESYAGCTRFGAALLVHEFFNDFQD
VLLVFSAIVFGAMAVGQVSSFAPDYAKAKVSAAHVIMIIEKIPLIDSYSTEGLMPNTL
EGNVTFNEVMFNYFTREDIFVLQGLSLEVKKGQTLALVGSSGCGKSTVVQLLERFYDP
MAGTVLLDGKEIKHLNVQMLEAHMGIVGSDFILFDCSIGENIAYGHDSURSVVSGEEIVR
AAKEANIHPFIETLPDKYNTRVGDKGTQLSGGQKQRIAIARALVRQPRILLLDEATSA
LDTBSEKVVQEALDXAR"
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INRLEEEMTTYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQILKIRKQFFHAIMRQEVG
WFDVHDVGELNTRLTDDVSKINEGIGDKIGWFFQSMATFFIGFIVGFTTGWKLTLVIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db xref="mariamycin-resistant subline of FT-1"
/cell_type="feline lymphoma cell line"
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/db_xref="GI:6472653"
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RESULT 10
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Method for predicting side effects
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JP 2002223769-A/1
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31-JAN-2001 JP 2001024723
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                                                                                                                                                                                                                                                        /organism='Homo sapiens (human)'
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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; Homo.
  PAT 07-JAN-2002
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and primer
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                                           Homo sapiens (human)
                                                                    BD190394 3988 bp [Phosphatidylcholine as a medicament BD190394 GI:33000133 JP 2002522381-A/1.
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Sequence 3 from Patent WO0192877.
AX322789
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 3988)
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Sorrentino, B. and Schuetz, J.

Method of identifying and/or isolating stem

Patent: WO 0192877-A 3 06-DEC-2001;

ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
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Method of identifying and/or isolating
Patent: WO 0192877-A 1 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (
Location/Qualifiers
1. .3860
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Mammalia; Eutheria; Primates;
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AX322787
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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07-JAN-2002

Euteleostomi;

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Length 3860;

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Length 3860;

for the protection of mucosa.

PAT 17-JUL-2003

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Phosphatialycholine as a medicament for the protection of the prot
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AR452556
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Patent: US 6677319-A 1 13-JAN-2004;
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Sequence 1 from Patent I
AX024454
AX024454.1 GI:10184622
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Stremmel,W.
Patent: DE 19857750-A 1 24-FEB-2000;
STREMMEL WOLFGANG (DE)
                                                                                                                                      Homo sapiens (human)
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Mammalia; Eutheria; Primates;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="genomic"
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Homo sapiens P-glycoprotein (mdr1)
AF016535
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2 (bases 1 to 4192)
2 (chen,G., Duran,G.E., Steger,K.A., Lacayo,N.J., Jaffred Chen,G., Duran,G.E., Steger,K.A., Lacayo,N.J., Jaffred Chen,C., and Sikic,B.I.

Multidrug-resistant human sarcoma cells with a mutant Multidrug-resistant human sarcoma cells with a mutant P-glycoprotein, altered phenotype, and resistance to J. Biol. Chem. 272 (9), 5974-5982 (1997)
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Chen,C.J., Chin,J.E., Ueda,K., Clark,D.
Gottesman,M.M. and Roninson,I.B:
Internal duplication and homology with
in the mdr1 (P-glycoprotein) gene from
                                                                                                                                                                                                                                                                                                                                                                              Chen.G., Lacayo,N.J., Steger,K.A. Direct Submission Submitted (28-JUL-1997) Medicine, Medicine, Stanford, CA 94306, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TREALDES I PVS FWRIMKLNLTEWPY FVVGVPCAI I NGGLQPAFAI I FSKI I GVFTKL
VTMQTRGINEVELEMADESKSE I DALEMSKSNDSRSSILTRKRSTRRS VRGSQADDRKLS
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I DDFETKRQNSNLFSLLFLALGI I SF I TFFLQGFTFGKAGEI LTRALR YNVFRSNLRQ
DVSWFDDFKNTTGALTTRLANDIDAQVKGAI GSRLAVTQON I ANLGTGI I I SF I YSWGL
TLLLLAI VPI I A I AGVVEMKMLSGQALKDKKELEGAGKI ATEAI ENFRTVVSLTQEQK
FEHMYAQSLQVVSYANGLOGVSSFADDYAKAKI SAHLI MI I EKTPLI DE YSTEGLMENTL
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LAGKVLLDGKEI KRLAVQMLRAHLGI VSQEPLI FDCS1 RENI AYGDNSRVVSQEEI VR
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Search completed: February 9, 2005, 17:02:01 Job time: 482.178 secs

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US-08-794-649A-1

US-08-794-649A-5

US-08-181-471-2

US-09-023-655-1167

US-09-033-276-18

US-08-583-276-18

US-08-583-276-11

US-09-316-167-1

US-09-316-167-1

US-09-397-233-1

5206352-3

5206352-3
                                                                                                                                                                                                     US-08-793-610-5

US-09-306-417-1

US-09-306-417-2

US-08-793-610-6

US-08-793-62-725C-1

US-09-672-725C-22

US-09-672-725C-24

US-09-672-725C-26

US-09-672-725C-3

US-09-672-725C-3
                                PCT-US94-06284-8
US-08-227-370-3
PCT-US94-06284-3
US-08-310-501-3
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Compugen Ltd
Sequence 1, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 1167, Ap
Sequence 18, Appli
Sequence 1, Appli
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Sequence 22, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 27, Appli
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69.6	70.4	71.2	71.2	72.8	72.8	72.8	72.8	72.8	72.8	74.4	74.4	76.0	76.0	76.0	76.0	87.2	87.2
616	945	26	26	47698	8137	1446	1255	723	601	3924	3924	3321	3321	3321	3321	4233	4233
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US-09-270-767-11434	US-09-134-000C-186	PCT-US94-06284-4	US-08-227-370-4	US-09-949-016-13514	US-09-566-921-7	US-08-787-091-1	US-09-949-016-1772	US-09-016-434-1422	US-09-949-016-61079	US-09-762-195-2	US-09-023-655-1168	US-09-970-966-175	US-09-825-294-175	US-09-713-550-175	US-09-640-173-175	US-09-450-105-1	US-09-120-513-1
Sequence 1143		۸. ۱			Sequence 7, A		٠,						Sequence 1/5,	Sequence 175,	Sequence 175,	; <u>-</u> -	۲,
11434, A	ddw 'a		4, Appli	514, A	/, Appii	Appii	/2, AD	22, Ap	61079, A	Z, Appli	1168, Ap	, -	•	s, App	•	ŕ	App 1 1

ALIGNMENTS

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APPLICANT: Stremmel, Wolfgang
TITLE OF INVENTION: Phosphatidylcholine as Medication with
TITLE OF INVENTION: Prosphatidylcholine as Medication with
FILE REFERENCE: 34691/208520
CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/8F99702426
PRIOR APPLICATION NUMBER: PS-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR APPLICATION NUMBER: 198 35 570.8 DE
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR SILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: Homo sapiens US-09-762-195-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 1
US-09-762-195-1/c
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US-08-784-649A-1/c
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Patent No. 6677319
                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08784649A Patent No. 5830697
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Best Local
                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT
TITLE OF INVENTION: CYCLOSPORIN MODULATION
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3988
  STREET: 2200
STREET: 2200
CITY: Menlo Park
CTATE: CA
                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 100.0%; Score 25; DB 4
Local Similarity 100.0%; Pred. No. 0.01;
1eb 25; Conservative 0; Mismatches
COUNTRY:
                                                                         ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1553
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

Floppy disk

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TELEFAX: 415-00- 10 NO: 5:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4264 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08784649A Patent No. 5830697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENERAL INFORMATION:
APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELECHONE: 415-322-5070
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sharwood, Pamela J
REGISTRATION NUMBER: REG.NO.
REPERENCE/DOCKET NUMBER: 060
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Menlo Park
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94025
                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                   415-322-5070
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                                                                                                                                                                                               5830697 36,677
                                                                                                                                                                                                                                                                                                                                                 Version
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US-08-181-471-2/c
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US-08-784-649A-5
                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-181-471-2
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                                                           Matches
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                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                      TELEFAX: 619-792-8477 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                              MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pair
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/041,553
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pitti-
                                                                                                                                                                  FEATURE:
                                                                                                                                                                                ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: AN TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Li, Lir
APPLICANT: Lishko,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 13-JAN-1994 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                             NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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STREET: 12526 High Bluff Drive, Suite 300
                                                                                                                                                                                                                               OPOLOGY:
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1911 GTGACATTTTCACGGCCATAGCGAA 1887
                                                           25;
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                 1 GTGACATTTTCACGGCCATAGCGAA 25
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METHOD FOR DELIVERING BENEFICIAL
METHOD FOR DELIVERING BENEFICIAL
MEMORITIONS TO HAIR FOLLICLES
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100.0%; Pred. No.
                                                                        100.0%;
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                                                          Score 25; DB
Pred. No. 0.0
0; Mismatches
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                                                                          .011;
                                                                                      Length 4646;
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US-09-023-655-1167/c
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HERFWTFFF.
CLASCTTOTE: HERFWTFFF.
                                                                                                                                                                                                                                           US-08-583-276-18/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1167, Application US/09023655 Patent No. 6607879
                                                                                                                                                                     Sequence 18, Application US/08583276
Patent No. 5837536
GENERAL INFORMATION:
Applitant
                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1167
                                    APPLICANT: Tolstoshev, Paul TITLE OF INVENTION: IMPROVED TITLE OF INVENTION: MULTIDRUG TITLE OF INVENTION: SELECTION NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cocks, Benjant.....
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilnamer
APPLICANT: TOURNTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: GENBA
                                                                                                                                              APPLICANT: McDonagh, Kevin T.
APPLICANT: Nienhuis, Arthur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: PALO ALTO
STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Zeller, Karen J. REGISTRATION NUMBER: 37,071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLONE: 9187468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                    1911 GTGACATTTTCACGGCCATAGCGAA 1887
                                                                                                                                                                                                                                                                                                                                                     1 GTGACATTTTCACGGCCATAGCGAA 25
                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4646 base pairs
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Carella, Byrne, Bain, Gilfillan,
Cecchi & Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                           MULTIDRUG
SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 4; 100.0%; Pred. No. 0.011;
                                                                           IMPROVED EXPRESSION OF HUMAN MULTIDRUG RESISTANCE GENES AND IMPROVED SELECTION OF CELLS TRANSDUCED WITH SUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1167:
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APPLICATION NUMBER: 08/332
FILING DATE: 31-OCT-1994
APPLICATION NUMBER: 07/887
APPLICATION NUMBER: 07/887
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08752447 Patent No. 5994088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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INFORMATION FOR SEQ ID NO: 1:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inc
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION WIMBER: US/08/752,447
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
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                                                                   ATTORNEY/AGENT INFORMATION:
NAME: NO. 5994088nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing
TITLE OF INVENTION: Using Immunoligcal Agents Specific
            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-9808
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 05-JAN-1996 CLASSIFICATION: 435
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OPERATING SYSTEM:
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
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25; Conserv
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300 South Wacker Drive, Seventh Floor
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ilarity 100.0%;
Conservative 0
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                                                                                                         Kevin E
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                                                                         95,1121
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for P-glycoprotein
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TOPOLOGY: linear MOLECULE TYPE: CDNA

STRANDEDNESS:

ະຣຣ: single linear

nucleic acid

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RESULT 8
US-09-316-167-1/c
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TELEPAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 base pairs
TYPE: nucleic acid
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Matches
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Patent No. 6365357
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APPLICANT: Mechetner, Eugene
APPLICANT: Roninson, Igor B
TITLE OF INVENTION: Methods a
TITLE OF INVENTION: Using Imm
                                                                                                                                                                                                                                          FILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6365357nan, Kevin I
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                 FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA;
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CORRESPONDENCE ADDRESS
                                                                                              OLECULE TYPE:
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LOCATION:
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STATE: Illinois
                                                                 NAME/KEY:
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CLASSIFICATION:
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 LOCATION:
                                                LOCATION:
                                                                                                                             STRANDEDNESS: single
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                                                                                                                 TOPOLOGY:
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25; Conservative
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425..4264
                                              5'UTR
1..424
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4265..4669
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1..424
CDS
425..4264
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                                                                                                  CDNA
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                                                                                                                                                                                                                                                                                                   Kevin E
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                                                              Query Match
Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: No. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-199
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                     LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mechetner, Eugene
TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunological Agents Specific for P-glycoprotein
                                                                                                                                                                                                         FEATURE:
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1911 GTGACATTTTCACGGCCATAGCGAA 1887
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                       1 GTGACATTTTCACGGCCATAGCGAA 25
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LOCATION:
                                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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STATE: Illinois
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                                                              100.0%; Score 25; Di
ilarity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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4265..4669
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425..4264
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1..424
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                                                                                  .011;
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5206352-3/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Michael M.
; TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS , NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:
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US-08-793-610-5/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5206352
APPLICANT: Roninson, Igor B., Pastan Ira H., Gottesman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. 5206352
APPLICANT: Roninson, Igor B., Pastan Ira H., Gottesman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:3:
                                                  Sequence 5, Application US/08793610

Patent No. 5858744

GENERAL INFORMATION:
GAPPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
APPLICANT: OSTERTAG, Wolfram
TITLE OF INVENTION: RETROVIRAL VECTOR HYBRIDS AND THE USE THEROF
TITLE OF INVENTION: FOR GENE TRANSFER
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
PRIOR DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                     NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4669
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                                                                                                                                                                                                                                                                                 1911
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Nikaido, Marmelstein, Murray & Oram LLF
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Pred. No. 0.0
0; Mismatches
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US-09-306-417-1/c
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                        SEQ ID NO 1
LENGTH: 8630
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09306417 Patent No. 6548301
                                                                                                                                                                                                                                               APPLICANT: Heinrich Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/793,610
FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (202)638-500
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-5704
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE COMPATI
NAME/KEY: misc_feature
LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
                                                                  FEATURE:
                                                                                 OTHER INFORMATION: Description of Artificial Sequence: proviral OTHER INFORMATION: plasmid DNA
                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                         TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 03 952.1
FILING DATE: 07-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/03175
                                                                                                                              FEATURE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-5701
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FILING DATE: 08-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Berman, Richard J. REGISTRATION NUMBER: 39,105
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TOPOLOGY: cir
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RESULT 14
US-09-306-417-2/c
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LENGTH: 8630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SFbeta71m4
                                                                       NAME/KEY: 5'UTR
LOCATION: (532)..(1219)
                                                                                                                               NAME/KEY: misc_feature
LOCATION: (161)..(677)
OTHER_INFORMATION: 5'-LTR
                                                                                                                                                                                                     LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
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LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
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LOCATION: (161)..(677)
                                                                                                                                                                                                                                                                                         OTHER INFORMATION: retroviral expression vector SFbeta91mSA1
                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(8630)
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OTHER INFORMATION: m4 mdr-1 cDNA
NAME/KEY: mat_peptide
LOCATION: (1220)..(5062)
DTHER INFORMATION: mSA1
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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LOCATION: (5215)..(5774)
DTHER INFORMATION: 3'-LTR
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les 25; Conserv
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ilarity 100.0%;
Conservative (
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   mdr1
   CDNA
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Pred. No. 0.012;
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US-08-793-610-6/c
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              Query Match
Best Local &
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APPLICANT: BAUM,
                                                                                                                                       TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid backbone (pUC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: DE 195 03 952.1
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP STREET: 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-FEB-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                              TOPOLOGY: ci
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 07-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                      NAME: Berman, Richar REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2706
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25; Conserv
l Similarity
25; Conserv
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                                                                                                                        nucleic acid
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                                                                                                                                        9318 base pairs
                                                                            circular
PE: DNA
                                                                                                                                                                                      (202) 638-4810
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                                                                                                                                                                                                                                                                   Richard
                                                                                                           double
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              100.0%; Score 25; DB 2; 100.0%; Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                  PCT/EP95/03175
                                                                                                                                                                                                                                                  39,105
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Pred. No.
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SUMMARIES

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Abk52041 cDNA enco	_						Aad38994 Human mor				Human	Adps4881 Human FRO	Human	Human				CUNA enc							Nazeso73 Himan MDR

ALIGNMENTS

AAD39002; .

23-SEP-2002 (first entry)

AAD39002 standard; DNA; 25

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                                                                                                                   WPI; 2002-471427/50.
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/note= "Phosphorothioate backbone"
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Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; ds.
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        Treating a subject (at multidrug resistance, e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAD39012 standard; DNA; 25 BP
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(RANK/) RANK D E
(HANZ/) HANZEL I
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                                                                                                                                                                                     New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
                                                                                                                                                                                                                                                                                                                                                         Penn
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Pred. No. 0.013;
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expression, co

Claim

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tissues.

SEQ ID NO 15991; 80pp; English

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and

isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alternative specific exon, it is genomic locus that includes their exon, in assessing alternative specific locus that includes their exon, in assessing alternative specific locus that includes their exon, in assessing

smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at

Sequence 219

seqdata.uspto.gov/sequence.html?DocID=20030194704

BP; 61 A; 56 C; 38 G; 64 T; 0 U; 0 Other;

DB 12;

Length 219;

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                                                                                                                                                      alternative
                                                                                                                                                              Human; probe; ss; gene expression; single exon probe; microarray;
                                                                                                                                                                                Human genome derived single exon probe #2291.
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GTGACATTTTCACGGCCATAGCGAA 344

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 15; SEQ ID NO 2291; 80pp; English

encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes is separately probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a method of probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an sequences (optionally with conservative amino acid substitutions), an

The invention relates to a nucleic acid probe for measuring human gene compression, comprising any of the 27,400 fully defined nucleotide encoding at least 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification, or their complements or fragments, and comprising a placat 8 amino acids of any of the 6888 amino acid sequences (fully defined in the specification. The probe is a single exon probe that compressed in human cells or tissues. Also included are a spatially-compressed in human cells or tissues. Also included are a spatially-defined sex probes in comprising a plurality of single exon nucleic acid compression of the plurality of probes is separately to gene expression (comprising a plurality of probes is separately conditions to an increasing human gene expression, a vector comprising the single exon nucleic acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acid subscription, and a computer-readable contiguous amino acid subscription, and a computer-readable than a customer destring to measure gene expression, a method of providing the above-methods and apparatus are useful in gene content according and characteristing according any of the above and apparatus are useful in gene content according and characteristing according and characteristing according and characteristing gross and provided according according

Sequence 584 BP; 166 A; 139 C; 100 G; 179 T; 0 U; 0 Other;

Matches Query Match 25; Similarity GTGACATTTTCACGGCCATAGCGAA 25 Conservative 100.0%; 0; Score 25; DB 12; Pred. No. 0.024; Mismatches 0 Length 584; Indels 0 Gaps

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PN WO2000 AAA96071 standard; DNA; 765 BP Drug resistance; ATP gradient; Human Pgp ATP binding cassette 29-JAN-2001 (first entry) human; ATP binding cassette; ABC transporter; chemotheraputic; (ABC) transporter coding sequence. antibiotic; herbicide;

WO200052144-A1

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2746/c
ACF62746 standard; DNA;
 New use of in subject !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   altering the ATP gradient across the biological membrane of the target cell. The method is useful for modulating drug resistance of cells. It useful for increasing the sensitivity of cells to chemotheraputic and antibiotic agents and increasing resistance to herbicides. The present sequence is human Pgp ATP binding cassette (ABC) transporter coding sequence. This sequence was used in the present invention to modulate drug resistance. Note: The present sequence is not shown in the specification, but is referred to via its GenBank accession number
                                                                                                         23-JUL-2001; 2001EP-00117608.
24-MAY-2002; 2002EP-00011710.
                                                                                                                                                                                                                                      cytochrome p450; cytostatic; gene;
                                                                                                                                                                                                                                                  Cancer; CYP3A5; irinotecan; pharmaceutical; malignant cytochrome p450; subfamily IIIA; nifedipine oxidase; p
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                                                                                                                                                                                                                                                                                    Cancer based on CYP3A5 related polynucleotide
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irinotecan for preparation of compositions for treating having genome with variant allele comprising cytochrome
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polypeptide
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                                                                                                                                                                          Use of irinotecan or its derivative for preparation of a pharmaceutical composition for treating cancer in a subject having a genome with a variant allele comprising a multidrug resistance protein 1 polynucleotide.
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lung cancer; ovarian cancer; pancreatic cancer;
variant allele; multidrug resistance protein 1;
                                                                                                                    Disclosure; SEQ ID NO
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24-MAY-2002; 2002EP-00011710.
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Pred. No. 0.026;
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MRP1; cytostati
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treating colorectal,

present invention describes a method for the use of irinotecan derivative for the preparation of a pharmaceutical composition ating colorectal, cervical, gastric, lung, ovarian or pancreatic

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Irinotecan; cancer; pancer;

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Colorectal cancer; colorectal cancer; pancer;

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COLORECTAL Cancer; pancer; colorectal cancer; colorectal cancer; colorectal cancer; colorectal cancer, colorectal 
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                                                                The invention relates to the novel use of irinotecan to treat a patient suffering from cancer. This involves determining if the patient has one or more variant alleles of the UGTIA1 gene, and if the patient has one or more of such variant alleles, irinotecan is administered in an increased or decreased amount in comparison to the amount that is administered without regard to the patient's alleles in the UGTIA1 gene. The invention has cyrostatic activity. A composition of the invention acts as a topoisomerase I inhibitor. The method is useful for treating a patient, an animal e.g. mouse or a human, preferably African or Asian, suffering from cancer such as colorectal, cervical, gastric cancer, lung, ovarian, pancreatic cancer or malignant glioma. The present sequence is udes in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irinotecan; cancer; UGTIA1; cytostatic; topoisomerase I inhibitor;
colorectal cancer; cervical cancer; gastric cancer; lung cancer;
ovarian cancer; pancreatic cancer; malignant glioma;
uridine diphosphate glycosyltransferasel member A1; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of irinotecan to treat cancer patient by determining if patient has variant alleles of UGTIA1 gene, administering increased/decreased amounts of irinotecan based on increased/decreased levels of UGTIA1 gene product.
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24-MAY-2002; 2002EP-00011710.
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                                                                                                                                                                                                                                                         colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The invention is useful for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject (preferably human, more preferably African or Asian) or a mouse. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to the novel use of irinotecan or its derivative for the preparation of pharmaceutical compositions for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 674; 130pp; English.
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24-MAY-2002;
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GTGACATTTTCACGGCCATAGCGAA
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ilarity 100.0%;
Conservative
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                                                                                                                                                                             BP; 224 A; 139 C; 182 G; 220 T; 0 U; 0 Other;
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2002EP-00011710.
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                                                                        Score 25; DB
Pred. No. 0.0
0; Mismatches
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Pred. No.
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malignant glioma;
; Cyp3A5; MRP1; MDR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 765;
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ABS65230//
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KW Huma:
KW phari
KW endo
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Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates ro a novel use of irinotecan or its derivative for the preparation of a pharmaceutical composition for treating colorectal, cervical, gastric, lung, ovarian or pancreatic cancer, or malignant glioma in a subject having a genome with a variant allele which comprises a multidrug resistance 1 (MDR1) polynucleotide. A composition of the invention has cytostatic activity. The present sequence is used in the
                                                                                                 Human; ss; gene; splice variant; tumour-involved gene; TIG; pharmaceutical composition; cancer; diagnostic; tumour; gen endothelial cell; cell differentiation; cell proliferation.
   04-JUL-2002.
                              US2002086384-A1
                                                          Homo sapiens.
                                                                                       gene
                                                                                                                                                             cDNA encoding tumour involved gene (TIG) splice variant, NV-31
                                                                                                                                                                                                                          ABS65230;
                                                                                                                                                                                                                                                      ABS65230 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New use of irinotecan for preparation of pharmaceutical compositions for treating cancer in subject having genome with variant allele comprising multidrug resistance 1 polynucleotide.
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24-MAY-2002;
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lung cancer; ovarian cancer; pancreatic cancer; malignant glioma;
multidrug resistance 1; MDR1; cytostatic; human; UGT1A1; MRP1; TOP1; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human MDR1 related DNA
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                                                                                       therapy.
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25; Conserv
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2002EP-00011710.
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                                                                                                                                                                                            (first entry)
                                                                                                   composition; cancer; diagnostic; tumour; gene therapy;
ll; cell differentiation; cell proliferation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 10
100.0%; Pred. No. 0.026;
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ABV78146

standard;

DNA;

0

15-NOV-2002

(first entry)

Human mdr-1

DNA SEQ ID NO 30

RNA inhibition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;

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cc variants that are all tumour-involved genes (TIGS). The nucleic acids and cc polypeptides are useful for determining the level of a nucleic acids and cc polypeptide in a biological sample, for detecting a variant nucleic acid or cc polypeptide sequence in a biological sample, for determining the level of variant nucleic acid or composition comprising the ratio between the level of variant sequence in a critical composition comprising and the level of the variant sequence from which cc the variant has been varied by alternative splicing in a second cc treating diseases (e.g. cancer) that can be ameliorated or cured by cincreasing or decreasing the level of the encoded protein. The nucleic acids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or cancer of the physiological function of the original The state or composition pharmaceuticals, for distinguishing various stages in the physiological function of the original Tig, in targeting or composition to cancer, for evaluating the state or compail, for determining mutations cancer stages in which cell cycle is non-cc finance therapy. The polypeptides are useful for identifying compounds capable of compoundate apoptosis either ex vivo or in vivo. The sequences presented in ABS65230-ABS65235 are the coding sequences for the new variants (NV) 1-cc and of the TiGs disclosed
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                             δ
                                                                                                                                  Matches
                                                                                             Query Match
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P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid sequence, which is an alternative splicing variant tumor involved genes, useful for detecting cancer, predisposition to cancer, for evaluating cancer state and in gene therapy for treating
                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses isolated human nucleic acid alternative splicing variants that are all tumour-involved genes (TIGs). The nucleic acids and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 60-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAR-2000;
16-MAY-2000;
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DB; ABG79700.
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DAVID A.
                                                                                Similarity
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                               GTGACATTTTCACGGCCATAGCGAA 25
                                                                                                                                  2307
GIGACATITICACGGCCATAGCGAA 1887
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                                                               Conservative
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2000IL-00136154
                                                                                                                                BP; 662 A; 441 C; 591
                                                                               100.0%; Score 25; 100.0%; Pred. No.
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                                                               0;
                                                                 Mismatches
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                                                                                                                                612 T; 0
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ABZ35722/c ID ABZ35722 standard; DNA; 3840 BP.
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RESULT 13
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asl) of dsRNA1 is complementary to (I) and at least part of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JAN-2001;
26-OCT-2001;
29-NOV-2001;
07-DEC-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibiting expression of target oncogenes, by administering doubt target and having an overhang.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-590671/63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JAN-2002; 2002WO-EP000152
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                                                                                                        Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; viru protozoacide; gene expression; antisense; tumour; infection; Plasm virus; viroid; anti-GPP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIBO-) RIBOPHARMA AG.
                                                                                                                                                                              Human mdr-1 polynucleotide SEQ ID NO
                                                                                                                                                                                                           07-FEB-2003
                                                    DE10100588-A1
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                    1484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 2001DE-01000586.
; 2001DE-01055280.
; 2001DE-01058411.
; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the invention
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene, useful e.g. for inhibiting ple-stranded RNA complementary to
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                                                                                                                                        Plasmodium;
                                                                                                                                                     virucide;
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09-JAN-2001; 2001DE-01000588

treating the

Inhibiting expression of target introduction of complementary do

et genes, e.g. oncogenes, in cells, b double-stranded oligoribonucleotide,

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after

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RESULT 14
ABX09965/c
ID ABX099
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ABX09967/c
ID ABX099
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AC ABX099
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DT 23-JAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 27-28; 100pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inhibiting expression of target genes, useful by introducing into cells two double-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-683450/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                             DE10100587-C1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human mdr-1 DNA fragment SEQ ID 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX09965;
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                                                                                                                                                                                                                                                                             09-JAN-2001; 2001DE-01000587.
                                                                                                                                                                                                                                                                                                                                09-JAN-2001; 2001DE-01000587
                                                                                                         WPI; 2002-742209/81.
                                                                                                                                                                                                                                                                                                                                                                                         21-NOV-2002.
                                                                                                                                                                Kreutzer R,
                                                                                                                                                                                                                         (RIBO-) RIBOPHARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  introducing into cells two the target.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGACATTTTCACGGCCATAGCGAA 1460
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tive 0;
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Pred. No. 0.036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3840;
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Disclosure; Page 32-33; 98pp; German.

target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention target gene by introducing into the cell that contains the target gene (ds) least one oligoribonuclectide (dsNAI) that has a double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of invention describes a novel method for inhibiting expression into the cell that contains the target ide (dsRNAI) that has a double-stranded gene (ds) at

Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

δ Query Match Best Local : Matches Н 25; Similarity GTGACATTTTCACGGCCATAGCGAA 25 Conservative 100.0%; 0; Score 25; DB 6; Pred. No. 0.036; Mismatches 6 0, Length 3840;

0

Gaps

0

유 1484 GTGACATTTTCACGGCCATAGCGAA 1460

ВP

ö 30

Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide; cytostatic; virucide; protozoacide; antibacterial; ds.

ά Hadwiger P;

Inhibiting gene expression in cells, useful for e.g. treating tumors, introducing double-stranded complementary oligoRNA having unpaired γď

104pp; German.

RESULT 15
ABL91687/c
ID ABL91687 standard; DNA; 3840 BP
XX
AC ABL91687;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human; HIV; HCV; gene expressic
KW Human; HIV; HCV; gene expressic
KW cytostatic; virucide; protozoac
XX
DE10100586-C1.
XX
PN DE10100586-C1.
XX
PN DE10100586-C1.
XX
PN DE10100586-C1.
XX
PN DE10100586.
XX
PR 09-JAN-2001; 2001DE-01000586.
XX
PR (RIBO-) RIBOPHARMA AG.
XX
PA (RIBO-) RIB The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for stranded segment of 1-4 nt. The method provides oligoribonucleotides for at

> និនិនិនិនិនិនិ but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. plasmodium or virtuses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration

Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T; 0 U; 0 Other;

Query Match Best Local Matches Local 25; Similarity Conservative 100.0%; 0 Score 25; DB 6; Pred. No. 0.036; Mismatches 6 0 Length 3840; Indels 0, Gaps

0

Search completed: February Job time : 245.69 secs 9 2005, 16:05:58

Job time :

Thu

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Published Applications NA:*

1: /cgn2_6/ptcdata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptcdata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptcdata/1/pubpna/US06_PUBCOMB.seq:*

6: /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

6: /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

7: /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*

10: /cgn2_6/ptcdata/1/pubpna/US09E_PUBCOMB.seq:*

11: /cgn2_6/ptcdata/1/pubpna/US09E_PUBCOMB.seq:*

12: /cgn2_6/ptcdata/1/pubpna/US09E_PUBCOMB.seq:*

13: /cgn2_6/ptcdata/1/pubpna/US09E_PUBCOMB.seq:*

14: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

16: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

17: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

19: /cgn2_6/ptcdata/1/pubpna/US10E_PUBCOMB.seq:*

20: /cgn2_6/ptcdata/1/pubpna/US10E_PUB.seq:*

20: /cgn2_6/ptcdata/1/pubpna/US10E_PUB.seq:*
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25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9, 2005, 13:42:02 ; Search time 266.667 Seconds (without alignments)
539.601 Million cell updates/sec
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(c) 1993 - 2005 Compugen Ltd
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Result No.	Score	Query	Query Match Length DB ID	DB	ID	Description
1	25	100.0	219	16	6 US-10-029-386-15991	Sequence 15991,
N	25	100.0	584	16	US-10-029-386-2291	Sequence 2291, A
c 3	25	100.0	2307	ဖ	US-09-805-020-31	Sequence 31, Appl
0	25	100.0	3840	18	US-10-384-339C-30	Sequence 30, App
ი თ	25	100.0	3860	ø	US-09-866-866A-1	Sequence 1, Appli
ი თ	25	100.0	3860	φ	US-09-866-866A-3	Sequence 3, Appli
c 7	25	100.0	4533	ဖ	US-09-805-020-30	Sequence 30, Appl
0 0	25	100.0	4643	13	US-10-072-621-2	Sequence 2, Appl
ი 9	25	100.0	4643	14	US-10-097-340-1	Sequence 1, Appl
c 10	25	100.0	4643	15	US-10-007-926A-258	Sequence 258, Ap
c 11	25	100.0	4646	11	US-09-968-007A-459	Sequence 459, Ap

ALIGNMENTS

RESULT 1
US-10-029-386-15991
; Sequence 15991, Application US/10029386
; Publication No. US20030194704A1

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US-10-029-386-15991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEGMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 15991
LENGTH: 219
Query Match
Best Local Similarity 100.
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                                                          FEATURE:

OTHER INFORMATION: MAP TO CHR7.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.6

OTHER INFORMATION: THIT: M29432.1, EVALUE 1.00e-120

OTHER INFORMATION: SWISSPROT HIT: B05183, EVALUE 8.00e-33

OTHER INFORMATION: EST_HUMAN HIT: BG567305.1, EVALUE 1.10e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank, David R.
Hanzel, David K.
                         100.0%; Score 25; DB 16; 100.0%; Pred. No. 0.016; tive 0; Mismatches 0;
                                                                                 Length 219;
                                 Indels
                                 <u>,</u>
                                 Gaps
                                 0;
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77

GTGACATTTTCACGGCCATAGCGAA

25

GTGACATTTTCACGGCCATAGCGAA 101

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US-09-805-020-31/c
; Sequence 31, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION NUMBER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
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Best Local S
Matches 25
                                                                       Matches
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2291, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FLING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K
                                                                                                                                                                      LENGTH: 2307
LENGTH: 2307
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
PAME/KEY: misc_feature
LOCATION: (1)...(2307)
OTHER INFORMATION: any n = a,c,g,t any unknown or other
                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1 EQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO CHR7.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN UNIQ, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: SWISSEROT HIT: POB183, EVALUE 4.00e-32
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                                                                                            Local Similarity
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1 GTGACATTTTCACGGCCATAGCGAA 25
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25; Conserv
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                                                                       Conservative
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                                                                                        100.0%; Score 25; DB 9; Length 2307; 100.0%; Pred. No. 0.025;
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US-10-384-339C-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-384-339C-30/c
                                                                                                                      US-09-866-866A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09866866A Patent No. US20020102244A1 GENERAL INFORMATION:
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Best Local Similarity 100.
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                                        Matches
                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
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                                                             Best Local
                                                                           Query Match
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR FILING DATE: 2002-01-09
PRIOR APPLICATION NUMBER: DE 10100586.5
PRIOR EILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR FILING DATE: 2001-10-26
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TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 20200/2002
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/866,866A CURRENT FILING DATE: 2001-08-30
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying
FILE REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sorrentino, Brian APPLICANT: Schuetz, John
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ORGANISM: Homo sapiens
PUBLICATION INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: DE 10160151.4
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                                                                                                                                                         LENGTH: 3860
TYPE: DNA
                                                                                                                                       ORGANISM: Homo sapiens
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  1 GTGACATTTTCACGGCCATAGCGAA 25
                                                           Similarity
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                                        Conservative
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100.0%; Pred. No.
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                                                         Score 25; DB 9;
Pred. No. 0.028;
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GTGACATTTTCACGGCCATAGCGAA 1463

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RESULT 7

US-09-805-020-30/c

; Sequence 30, Application US/09805020

; Dublication No. US20020086384A1

; GENERAL INFORMATION:

; APPLICANT: LEVINE, Zurit

TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES

; FILE REFERENCE: 2786-0168P

; CURRENT APPLICATION NUMBER: US/09/805,020

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 30

; FURTURE OF SEQ ID NOS: 72
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; Sequence 3, Application US/09866866A
; Patent No. US20020102244A1
; GENERAL INFORMATION:
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, NAME/KEY: misc_feature
, LOCATION: (1). (4533)
, OTHER INFORMATION: any n = a,c,g,t any unknown or other
US-09-805-020-30
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RESULT 4

US-10-072-621-2/c

US-10-072-621-2/c

; Sequence 2, Application US/10072621

; Publication No. US20020169137A1
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LENGTH: 3860
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TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/99/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-08-36
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1999-05-27
PRIOR FILING DATE: 1998-05-28
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Best Local Similarity
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ORGANISM: homo sapiens
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TYPE: DNA
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Local Similarity 100.0%; Pred. No. 0.028;
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Pred. No.
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SEQ ID NO 2
LENGTH: 4643
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-097-340-1
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Matches 25;
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                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 1
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APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR I
FILE REPERENCE: 100103.402
CURRENT PILING DATE: 2002-03-08
UMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REFERENCE: WRI-030 CURRENT FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: 60/276,025 PRIOR FILING DATE: 2001-03-14 PRIOR APPLICATION NUMBER: 60/276,025 PRIOR FILING DATE: 2001-03-25 PRIOR APPLICATION NUMBER: 60/325,149 PRIOR APPLICATION NUMBER: 60/276,026 PRIOR APPLICATION NUMBER: 60/324,967 PRIOR APPLICATION NUMBER: 60/311,732 PRIOR APPLICATION NUMBER: 60/311,732
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APPLICANT:
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APPLICANT: Manjula GANN
APPLICANT: Sebastian HO
                                                                                                                         PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
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Xumei ZHAO
Karen GLATT
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Rachel E. MEYERS
Michael MORRISEY
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Shubhangi KAMATKAR
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Robert C. BAST, Jr
Karen LU
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ilarity 100.0%;
Conservative 0
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Pred. No. 0.028;
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RESULT 11
US-09-968-007A-459/c
; Sequence 459, Application US/09968007A
; Publication No. US20040115625A1
; Publication No. US20040115625A1
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CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
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                                                                       TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Usining Signa Title OF INVENTION: Gene Sets FILE REFERENCE: 689290-71
CURRENT APPLICATION NUMBER: US/09/968,007A
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HOULGATTE, REMI
APPLICANT: BIRNBAUM, DANIEL
APPLICANT: NGUYER, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REFERENCE: 1546-R-00
                                                       PRIOR APPLICATION NUMBER: US/60/237,316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BERTUCCI, FRANCOIS APPLICANT: HOULGATTE, REMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1908 GTGACATTTTCACGGCCATAGCGAA 1884
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ING DATE: 2000-10-02
SEQ ID NOS: 1001
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o. US20030143539A1
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(mdr/tap), member 1 (ABCB1) gene.
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Pred. No. 0.028;
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Pred. No. 0.028;
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US-10-641-643-1167/c
US-10-641-643-1167/c
Sequence 1167, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:

APPLICANT: Cocks, Benjamin G. Susan G. Stuart

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
STREET: 3174 PORTER DRIVE

STATE: CALIFORNIA COUNTRY: USA ZIP: 94304

CITY: PALO ALTO

NUMBER OF SEQUENCES: 1508

TITLE OF INVENTION: COMPOSITION FOR GENE EXPRESSION

Jeffrey J.

Seilhamer

THE DETECTION OF BLOOD CELL

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                                                                                                                                                                ; TYPE: DNA; Homo sapiens US-09-968-007A-747
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CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US/60/237,172
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PELICATION NUMBER: US/60/237,278
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR PILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR PILING DATE: 2000-10-02
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US-09-968-007A-747/c
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APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination
TITLE OF INVENTION: Gene Sets
FILE REFERENCE: 689290-71
                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1001
SOFTWARE: PatentIn version 3.0
SEQ ID NO 747
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Publication No.
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Best Local Similarity
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1911 GTGACATTTTCACGGCCATAGCGAA 1887
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25; Conserv
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o. US20040115625A1
                                                                                  Conservative
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                                                                                                     100.0%; Score 25; 100.0%; Pred. No.
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APPLICANT: Roninson, Igor B.

APPLICANT: Ruth, Adam

TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that Improve Its

TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs

FILE REFERENCE: 00,616-A

CURRENT APPLICATION NUMBER: US/10/343,657

CURRENT ETLING DATE: 2003-10-17

PRIOR APPLICATION NUMBER: 60/222,313

PRIOR FILING DATE: 2000-08-01

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGUTH: 4646

TYPE: DNA

ORGANISM: Homo sapiens
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US-10-343-657-1/c
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WOR'D PERFECT 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WOR'D PERFECT 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WOR'D PERFECT 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WOR'D PERFECT SOFT INFORMATION

APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION NUMBER: -Unknown>
PRIOR APPLICATION NUMBER: -Unknown>
PILING DATE: -Unknown>
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 37,071
REFERRENCE/DOCKET NUMBER: 37,071
REFERRENCE/DOCKET NUMBER: 37,071
REFERRENCE/DOCKET NUMBER: 58,001
REFERRENCE/DOCKET NUMBER: ST.001
REFERRENCE/DOCKET NUMBER: 
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; NAME/KEY: CDS
; LOCATION: (425)..(4264)
US-10-343-657-1
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Best Local S
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Best Local
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1es 25; Conservative
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SEQUENCE DESCRIPTION: SEQ ID NO: 1167:
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    1911 GTGACATTTTCACGGCCATAGCGAA 1887
                                                                        1 GTGACATTTTCACGGCCATAGCGAA 25
                                                                                                                                            ch 100.0%; Score 25; DB 17; Length 4646; Similarity 100.0%; Pred. No. 0.028; 25; Conservative 0; Mismatches 0; Indels 0
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TYPE: nucleic acid
STRANDEDNESS: single
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RESULT 15
US-10-775-169-198/c
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Publication No. US20040175743A1
                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.2
SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wyeth
APPLICANT: Burcz;
APPLICANT: Twine
APPLICANT: Dorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                             Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                          APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AM101080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
                                                                                                                   Query Match
                                                                                                                                                                                LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
1911 GTGACATTTTCACGGCCATAGCGAA 1887
                                       1 GTGACATTTTCACGGCCATAGCGAA 25
                                                                         100.0%; Score 25; DB 18; ilarity 100.0%; Pred. No. 0.028; Conservative 0; Mismatches
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Search completed: February 9, 2005, 22:26:40 Job time: 267.667 secs

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No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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ALIGNMENTS

RESULT 2 AY408954/c LOCUS DEFINITION	Qу	Query Match Best Local : Matches 2:	ORIGIN		source	FEATURES		COMMENT	JOURNAL	TITLE	20110110	REFERENCE		ORGANISM	KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1 BP220580/c
AY408954 3843 bp DNA linear GSS 15-DEC-2003 Homo sapiens ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	1 GTGACATTTTCACGGCCATAGCGAA 25 	Query Match 100.0%; Score 25; DB 5; Length 570; Best Local Similarity 100.0%; Pred. No. 0.25; Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		/olganiam- nome of particle / noll type="manA no. / no. / type="manA no. / no.		Location/Qualifiers	Department of Medical Science, University of Tokyo Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedal, Minatoku, Tokyo 108-8639, Japan Email: ysuzuki@ims.u-tokyo.ac.jp.	Contact: Yutaka Suzuki	Genome Res. 14 (9), 1711-1718 (2004)	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	•	I (bases 1 to 5/0) Suruki V. Yamashita.R Shirota.M., Sakakibara,Y., Chiba,J.,	Eukaryota; Metazoa; Choroata; Craniata; verteurata; Eutereoscomi, Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.		EST:	BP220580 1 GT.52091485	BP220580 Sugano cDNA library, colon Homo sapiens cDNA clone COL03695, mRNA sequence.	

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                                                                                                                                                                                                    Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., St Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp
                   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/locus_tag="HCM3396"
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tive 0; Mismatches 0
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TRANSCRIPT, partial sequence.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2492 row: c column: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 929)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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AGENCOURT 8627902 NIH MGC 43
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This sequence was made
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                  Similarity
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 GTGACATTTCACGGCCATAGCGAA 25
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Location/Qualifiers
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based on alignment
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                                  Conservative
                                                                                                                  /tissue_type="normal pigmented retinal epithelium"
/lab host="DH10B (phage-resistant)"
/clome lib="NIH MGC 43"
/clome lib="NIH MGC 43"
/clome lib="NIH MGC 43"
/clome lib="NIH MGC 43"
/clomed into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. | "
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/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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|mol_type="genomic DNA"
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100.0%; Pred.
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                                               Score 23.4; DI Pred. No. 1.7;
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RESULT 5
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SOURCE
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BI184814
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                                                                                                                                                                                                                                                                                                                                                                                                                                            239 GTGACGTTTTCTCGGCCATAGCGAA 215
Contact: Pomp, D
Department of Animal Science
University of Nebraska, Lincol
Lincoln, NE 68583-0908, USA
Tel: 402 472 6416
Fax: 402 472 6362
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One Amgen Center.
Tel: 805 447-4881

Plate: 00278 row: b column: 7.
Plate: Location/Qualifiers
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AMGNNUC:NRHY5-00278-B7-A W Rat hypothalamus (10471) Rattus
norvegicus cDNA clone nrhy5-00278-b7 5', mRNA sequence.
CB727009
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                            Sus scrofa
Sus scrofa
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Amgen EST Program
Amgen Rat EST Program
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UNL-P-FN-cr-g-09-0-UNL.81 UNL-P-FN Sus scrofa
UNL-P-FN-cr-g-09-0-UNL 3', mRNA sequence.
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                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; (Dases 1 to 784)
Caetano, A. R., Johnson, R. K. and Pomp, D. Generation and sequence characterization of a normal library from swine ovarian follicles
Mamm. Genome 14 (1), 65-70 (2003)
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BI184814.1 GI:14659223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="nrhy5-00278-b7"
/clone lib="W Rat hypothalamus (10471)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1;
hypothalamus adult female Wistar rat avg. insert sikb fraction 6 and 7"
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/mol_type="mRNA"
/db_xref="taxon:10116"
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92.0%;
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Pred. No. 9.5;
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Seg primer: M13 -29
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
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                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov plate: LLAM9798 row: 1 column: 02
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/dev_stage="ADULT"
/lab_host="DH10B [Life Technologies)"
/lab_host="DH10B [Life Technologies)"
/lab_host="UNL-P-FN"
/clone [lib="UNL-P-FN"
/clone | The UNL-P-FN"
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Location/Qualifiers
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/strain="University of Nebraska, Lincoln Swine Selection
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/mol_type="mRNA"
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clone="UNL-P-FN-cr-g-09-0-UNL"
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/clone="IMAGE:4218385"
/lab_host="DH10B (T1 phage-resistant)"
                                                                             /db_xref="taxon:10090"
                                                                                                            /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                           1. .894
                                                                                                                                                                           organism="Mus musculus"
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Ca. Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozai Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasuka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                            Group Phase I & II Team.
Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new capacity of the control of the control of the control of the capacity of t
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3182 bp mRNA linear HTC 03-F MNB musculus 11 days pregnant adult female ovary and uterus RIKEN full-length enriched library, clone:5031438E12 product:ATP-binding cassette, sub-family B (MDR/TAP), member
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="Organ: colon; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (650 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yoko Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.jp, Kanagawa 230-0045, Japan (B-m
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo. Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; (bases 1 to 3816)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, J. Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                             Science 302
                                                                                                          gene trios
                                                                                                                                               Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus
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URL:http://fantom.gsc.riken.jp/.
Location/Qualifiers
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Encyclopedia Project of Genome Exploration Research Group Genomic Sciences Center and Genome Science Laboratory in I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA library was prepared and sequenced in Mouse Genome
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Fax:81-45-503-9216)
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member 1B (MGD|MGI:97568, GB|NM_011075,
99%, match=2587)"
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/mol_type="mRNA"
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/clone_Tib="RIKEN full-length enriched
/dev_stage="11 days pregnant adult"
1. .3182
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/db_xref="taxon:10090"
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPCI44_284D11.r RPCI-44 Sus scrofa
genomic survey sequence.
CL388323.1 GI:51440283
                                                                                                                                                                                                                                                                                                                                                                                                                   Other GSSs: RPCI44 284D11.f
Contact: Lawrence B. Schook
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 265 5326
Fax: 217 244 5617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 411)

Rogatcheva,M.B., Meyers,S., He,W., Larkin,D.M., Marron,B.M., Beever,J.E. and Schook,L.B.

Piggy-BACing the Human Genome: Constructing a Porcine Physical Map Through Comparative Genomics
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                                                                                                                                                                                                       Clones are derived from the porcine BAC library RPCI-44 (http://www.bacpac.chori.org/porcine242.htm). For BAC library availability, please contact Pieter de Jong (pdejong@chori.org). Clones may be purchased from BACPAC Resources (http://BACPACorders.chori.org). This work was undertaken as part of the International Swine Genome Sequencing Consorrium by University of Illinois at Urbana Champaign, USA with funds provided by grant No. AG2002-34480-11828 from USDA-CSREES and AG2001-35205-09965 from USDA/NRI (Livestock Genome Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                   Email: schook@uiuc.
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/mol_type="genomic DNA"
/strain="four pigs (breed: 37.5% Yorks Landrace and Meishan)"
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/locue_tag="HCM3396"
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/mol_type="genomic DNA"
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                                                               /organism="Sus scrofa"
                                                                                       1. .411
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1 (bases 1 to 674)

1 (bases 1 to 674)

1 noardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs (curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BU437349 674 bp m 604145918F1 CSEQREN11 Gallus gallus
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Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12445392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                   /clone lib="CSEQRBN11"
//clone lib="CSEQRBN1"
Site 2: Notl; This normalized library was constructed from lilion independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoXI, size-selected, and cloned into the NotI and EcoXI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone lib="RPCI-44"
/note="Vector: pTARBAC2; Site_1: EcoRI; Site_2: EcoRI;
porcine male BAC library produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9823"
/clone="RPCI44_284D11"
a significantly longer reannealing hybridization was
                                                                                                                                                                                                                                                                                                                      /tissue_type="muscle"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Layer and broiler"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                        clone="ChEST986c5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GI:25926660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20.2; Depred. No. 57; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nRNA linear EST 29
CDNA clone ChEST986c5
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ORIGIN

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AUTHORS
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BU239912/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
MEDLINE
PUBMED
                                                                                          Query Match
Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PO Box 88, Manchester, M60 1QD, Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 716)

Boardmann, P.E., Sanz-Ezquerro, J., Overton, I.M., E

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.

A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BU239912.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr.
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                                    GTGACATTTTCACGGCCATAGCGAA
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                                                                                                                                                           /clone_lib="CSEQCHN33"
/clone_lib="CSEQCHN33"
/note="Organ: liver; Vector: pBluescript II KS(+); Site_1:
/note="Organ: liver; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simon.Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'sex≃"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="ChEST250k17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Gallus gallus"
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                                                                                        80.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 host="DH108"
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                                                                      Score 20.2; I
Pred. No. 64;
0; Mismatches
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Pred. No. 63;
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gallus cDNA clone ChEST250k17 5', mRNA
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                                                                                                           Length 716;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Technology
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                                                                      Gaps
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JOURNAL COMMENT
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AUTHORS
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CD251708/c
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
ORGANISM
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AUTHORS
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ORGANISM
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VERSION
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BP261688/c
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                                                                                                                                                                                                                                                                                         TITLE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545 TGACATTTTCACGGGCATACCGA 523
                                                                                                                                                                  Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                 1 (bases 1 to 923)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: NDAM449 row: d column: 08
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                          CD251708.1 GI:31012174
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD251708 923 bp
AGENCOURT 14205957 NIH MGC 179 Ho
IMAGE:30384175 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Virology
Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Jag Email: ysuzuki@ims_u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 578)
Suzuki,Y., Yamashita,R., Shirota,M., Sakakil
Mizushima-Sugano,J., Nakai,K. and Sugano,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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BP261688.1 GI:52176919
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BP261688 Sugano cDNA library, successor of the sugano cDNA library.
High quality sequence start: 2
                                                                                                                                                  Tissue Procurement: Dr. Michael Brownstein
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                         cDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGACATTTTCACGGCCATAGCGA 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="small intestine"
/clone_lib="Sugano cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="HSI04571"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.2%;
91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 19.8; D
Pred. No. 97;
0; Mismatches
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12185 row: f column: 23
High quality sequence stop: 495.
Location/Qualifiers
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1 (bases 1 to 1235)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
  21; Conservative
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/mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
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/lab host="MAGE:30384175"
/lab host="MH10B-Ton A ( T1 and T5 phage resistances)"
/lab host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone_11b="NIH_MGC_179"
/clone_11b="NIH_MGC_179"
/destroyed); Site_2: Not1; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MGC_71"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb. "
                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
79.2%; Score 19.8; DB 4; 91.3%; Pred. No. 1.1e+02; tive 0; Mismatches 2;
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Search completed: February 9, 2005, 21:55:42 Job time : 2450.85 secs

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Post-processing: Minimum Match 0%
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 nucleic search, using sw model
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Copyright (c) 1993 - 2005 Compugen Ltd.
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25 bp from Patent WO0234291.	ALIGNMENTS	108557	AR091275		HUMMDR1	AX504298	AX391099	AX336708	AX336420	AR380622	149610	CQ861565	BD234195	AX587788	AX522070	CQ815440	CQ716151	E02326	AR051650	AR051647	AX108656	AR399195	AF016535	AX108654	AR399194	AX024454	AR452556	
DNA																												
linear		1085	AR0912	AR05	M1475		AX39			AR380	I496:	CQ86:	BD23	AX58	AX522070	CQ81:	CQ716	E023	AR051	AR051	AX108	AR399	AFOI	AX108	AR399	AX024	AR452	
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27-SEP-2002		equence 3	Sequence	Sequence	Homo sapien	Sequence	Sequence	Sequence	Sequence	Sequence	equence 2	Sequenc		Sequence	Sequence		Sequence	Multidrug r		Sequence		Sequence	Ното варт	Sequ				

RESULT 2 AX504328/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Q Q	Query Match Best Local Matches 2	source	JOURNAL FEATURES	REFERENCE AUTHORS TITLE	SOURCE ORGANISM	AX504311 LOCUS DEFINITION ACCESSION VERSION
AX504328 25 bp DNA linear PAT 27-SEP-2002 Sequence 31 from Patent WO0234291. AX504328 AX504328.1 GI:23386140 Homo sapiens (human)	GAACCAGGGCACGTGCAATGGC 	Y Match 100.0%; Score 25; DB 6; Length 25; Local Similarity 100.0%; Pred. No. 0.89; nes 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	/organism="Homo sapiens" /organism="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"	multiple drug resistance Patent: WO 0234291-A 14 02-MAY-2002; THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) Location/Qualifiers	1 Colgan, S.P. Compositions and methods for treating hematologic malignancies and	Homo sapiens (human) Homo sapiens Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	AX504311 25 bp DNA linear PAT 27-SEP-2002 Sequence 14 from Patent WO0234291. AX504311 AX504311.1 GI:23386129

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                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic organization of the human multidrug resistance (MDR1) gene and origin of P-glycoproteins
J. Biol. Chem. 265 (1), 506-514 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 215) Chen,C.J., Clark,D., Ueda,K., Pastan,I., Gottesman,M.M. and Roninson,I.B.
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Human P-glycoprotein (MDR1) gene,
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Patent: WO 0234291-A 31 02-MAY-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
Location/Qualifiers
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M29433.1 GI:187482
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/db_xref="taxon:9606"
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/number=14
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BB171402 3843 bp
Method for predicting side effects
used therefor.
BD171402
BD171402.1 GI:28412692
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                                                                                                                                                                                                                                                                                             Kreutzer,R., Limmer,S., Rost,S. and Hadwiger,P. Method for inhibiting the expression of a target gene Patent: WO 02055693-A 30 18-JUL-2002; Ribopharma AG (DE)
                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bhattnagar, S.K., George, A.L. Jr. and Nazarenko, I.
Amplification of nucleic acid sequences
Patent: US 5593840-A 1 14-JAN-1997;
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                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
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/mol_type="unassigned
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AF537133/c
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Mammalia; Eutheria; Primates;
1 (bases 1 to 3843)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent: JP 2002223769-A 1 13-AUG-2002;
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AF537133.1 GI:22775295
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Hanscom, S.R., Xiao, G. and Crespi, C.L.
Rhesus monkey P-glycoprotein mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                             MA 01801,
                                                                                                                                                                          Submitted (09-AUG-2002) BD Biosciences,
                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                  2 (bases 1 to 3852)
Hanscom, S.R., Xiao, G. and Crespi, C.L.
                                                                                                                                                                                                                                                                                    Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                             Macaca mulatta
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ICHIRO IBIRI
C12N15/09,C12Q1/68,C12N15/00
Method for predicting side e
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JP 2002223769-A/1
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1.3852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism='Homo sapiens
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                                                                                                                                                               USA
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Pred. No. 0.7
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                                       p-glycoprotein"
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25; Conserv
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Stocker, P.J., Steimel-Crespi, D.T., Xiao, G.
Direct Submission
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AF537134
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On Jun 6, 2003 this sequence 
Location/Qualifiers
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Stocker, P.J., Steimel-Crespi, D.T., Xiao, G. and Crespi, C.L.
Cynomologous monkey P-glycoprotein mRNA
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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GNLEFRIVIHESY PSREWKILKGLINLKVQSGQTVALVCHSGCKSTTVQLMQRLYDF

GNLEFRIVIHESY PSREWKILKGLINLKVQSGQTVALVCHSGCKSTTVQLMQRLYDF

EGNAYDF INKLEQKFEDTLVGERGAQLSGGCKORI AI ARALVRNEKILLLDEATSALDT

ESRAVQVALDKARKGRTTI VI AHRLSTVRNADVI AGFBDUV VEKGHIÐELMKERGI

YKLVTMQTAGNE I ELENAADESKSE IDTLEMSSHDGGSSLIRKGSTRREVRESGOGD

YKLSTKEALDES I ÞPUSFMRINKLINLTEMPYFVVGVFCAI INGGLQÞAFAVI FSKI IG

I FFRNDDATKRQNSNLFSLLFLVGI VSFI FFFLQFFFFGKAGEILTKRLKYMVFRS

MLRQDVSWFDDPKNTTGALTTRLANDAAQVKGAI GSRLAI ITQNI AILGTGI I 15LLI Y

GWQJTLLLAI VDF I AI AGVUSMKMLSGQALKDKKELEGAGKI ATEAI EN FRTVVSLT

QEQKFEHMYDQSLQVPYRNSLRKAH I FGI TESFTQAMYFSY YAGCFRFGAYLVAHSIM

SFEDVLLLVFSAVVFGAMAVGQVSSFANDYAKAKVSAAHI IMI I EKTPLI DSYSTTGGLK

PNTLEGNTTFRUDGKEI KQLNVQWLRAHLGI USGEP ILFDCSI SENN AYGONSRVVSQE

FYDPLAGKVLLDGKEI KQLNVQWLRAHLGI USGEP ILFDCSI SENN AYGONSRVVSQE

FYDPLAGKVLLDGKEI KQLNVQWLRAHLGI USGEP ILFDCSI SENN AYGONSRVVSQE
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DTVPVMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMR
QEIGWFDVHDVGELNTRLTDDVSKINEGIGKKIGMFFQSMATFFTGFIVGFTRGWKLT
LVILAISPVLGVSAAAWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKE
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ATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQQ
LLAQKGIYFSMVSVQAGAKRQ"
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                                                                                                                                       tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:31442762
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Pred. No. 0.78;
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RESULT 8

DEFINITION AF537134/c

Snoo

ORIGIN

Best Loc Matches

REFERENCE AUTHORS TITLE JOURNAL

REFERENCE

AUTHORS TITLE

JOURNAL

REMARK COMMENT

FEATURES

SdD

REFERENCE AUTHORS TITLE

JOURNAL

VERSION KEYWORDS

ORGANISM

ACCESSION

QEIGMFDVHDVGELNTRLTDDVSK.INEGIGDK.IGMFFQSMATFFTGFIVGFTRGWKLT LVILAISFVLGLSAAVWAKILSSFTDKELLAYAKAGAVAEEVLAAIRTVIAFGGQKKS /translation="MDLEGDRNGGAEKKNFFKLNNKSKKDKKERKPTVSVFSMFRYSN WLDKLYMVVGTLAAIIHGAGLPLMMLVFGDMTDTFANAGNLGDLGALLFNNTNSSNIT DTVPVMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMR

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AY582534/c
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Booth-Genthe, C.L., Roller, C.R.
Cloning of Macaca mulatta MDR1
                                                                                                                                                                                                                                                                                                                                                                                      Laboratories, WP75A-203, West
Location/Qualifiers
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Booth-Genthe, C.L., R
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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EGMYSVDGGDIRTINVRFLREIIGVVSGEPULFATTIALBIRTSKEDYTMDEIEKAVK
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ESEAVVQVALDKARKGRTTIVIAHRLSTVRNADVIAGFDDGVLVEKGHBDELMKEKGI
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IFTRNDDAETKROKNLFSLLFLYLGIVSFITFFLOGETFGKAGEILTKRLSTWRPRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission
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/db_xref="GI:46394984"
/translation="MDLEGDRNGGAEKKNFFKLNNKSKKDKKERKPTVSVFSMFRYSN
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DTVPVMNLEEDMTRYAYYYSGIGAGVLVAAYIQVSFWCLAAGRQIHKIRKQFFHAIMR
                                                                                                                                                                                                                                                                       /mol_type= ".........9544"
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                                                                                                                                            codon_start=
                                                                                                                                                                                                                                         'gene="MDR1"
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Pred. No. 0.78;
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ESEAVVOVALDKARKGRTTIVIAHRLSTVRNÄDVIAGFDDGVIVEKGNHDELMKEKGI
FRKLYMYGTAGNEIELENAADESKSEIDTLEMSSHDSGSSLIAKRSTRRSVRGSGOD
RKLSTKEALDESIPVSFRRIMKLLITEMSYEVGVGVCAIINGGLOPAFAVIFSKIIG
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ETVRAKKEANIHAFIESISLANKYSTRYGDKGFOOLSGOKORIAIRALLVROHIILLID
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EGMYSVDGQDIRTINVRFLREIIGVVSQEPVLFATTIAENIRYGREDVTMDEIEKAVK
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LVILAISPILGLSAAAWAKILSSFTDKELLAYAKAGVVAEPULAAIRTVIAFGGOKKE
LERYNKNLEBAKRIGIKKAITANISIGAAFILIYASYALAFWYGTTLVLSKEYSIGOV
LTVFFSVLIGAFSVGQASPSIEAFANARGAAFEIFKIIDNKPSIDSYSKSGHKPDNIK
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                                                    ATSALDTESEKVVQEALDKAREGRTCIVIAHRLSTIQNADLIVVFQNGRVKEHGTHQC
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ORIGIN

Matches

25;

Conservative

0;

Best Local Query Match

Similarity

100.0%; 100.0%;

Score 25; Pred. No. Mismatches

0.78; DB 9;

Length 3852;

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DEFINITION ACCESSION
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             Homo sapiens (human)
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Sequence 1 from Patent WO0192877.
AX322787
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                        AX322789.1 GI:18093767
                                                                                               AX322789
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Sorrentino, B. and Schuetz, J.

Method of identifying and/or isolating stem

Patent: WO 0192877-A 1 06-DEC-2001;

ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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                                                                     3860 bp
from Patent WO0192877
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100.0%; Pr
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Pred. No. 0.7
D; Mismatches
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BD190395/c
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BD234199/c
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                                                                                                                                                                                                                                                                                                                                                                                                      Phosphatidylcholine as a medicament for the preparent JP 200252381-A 2 23-JUL-2002;

Wolfgang STREMMEL
OS Homo Sapiens
PN JP 200252381-A/2
PD 23-JUL-2002
PF 06-AUG-1999 JP 2000563262
PR 06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DI wolfgang stremmel
CC
FH Key Location/Qualifiers.
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Phosphatidylcholine as a m
BD190395
BD190395.1 GI:33000134
JP 2002522381-A/2.
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Method of identifying and/or isolating
Patent: WO 0192877-A 3 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (
Location/Qualifiers
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                                       BD234199

3924 bp DNA linear PAT 17-JUL-2003 ATP-binding cassette genes and proteins for diagnosis and remedy of light disorders and inflammatory diseases.

BD234199

BD234199.1 GI:33043969

JP 2002525111-A/9.
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            Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                       Similarity
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06-AUG-1998 DE 198 35 526.2,15-DEC-1998 DE 198 57 750.8 PI
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medicament
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                                          RESULT 15
AR452557/c
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1 (bases 1 to 3924)
3 Schmitz,G. and Klucken,J.
3 ATP-binding cassette genes and proteins for dii
1ipid disorders and inflammatory diseases
Patent: JP 2002525111-A 9 13-AUG-2002;
BAYER AKTIENGESELLSCHAFT
OS Homo sapiens (human)
PN JP 2002525111-A/9
PD 13-AUG-2002
PF 21-SEP-1999 JP 200572359
PF 21-SEP-1999 US 60/101706
PR GERD SCHMITZ, JOCHEN KUICKEN
PC C12N15/09,A61X38/00,A61X45/00,A61X48/00,A6
PA 6129/00,
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Sequence 2
AR452557
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C12P21/02,C12Q1/68,
PC G01N33/53,C12N15/00,C12N5/00,A61K37/02
CC human cDNA of ABCB4 (MDR3)
FH Key Location/Qualifiers
FT Source 1,3924
FT fource forganism='Homo sapiens
                                                                                                                                                                   25;
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
Compositions for the detection of blood cell
response gene expression
Patent: US 6607879-A 1168 19-AUG-2003;
Location/Qualifiers
                                                                                                                                     1 CGAACCAGGCACGTGCAATGGCGA 25
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25-SEP-1998 US 60/101706
GERD SCHMITZ, JOCHEN KLUCKEN
C12N15/09, A61K38/00, A61K45/00, A61K48/00, A61P3/06, A61P9/10,
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                                  PAT 20-FEB-2004
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Maximum Match 100%
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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SUMMARIES

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LSIBY, A	ys, Appr	TOSO, AD	yz, Appı	760, App	/69/, AD	2//9, AP	9462, AP	9372, AD	9404, AD	1/216, A	15657, A	191244,	191243,	100%, AD	1, WDD11	TIGGE	11000

ALIGNMENTS

CORRESPONDENCE ADDRESS: ADDRESSEE: ODGORPHARM, Inc. STREET: 200 Perry Parkway CITY: Gaithersburg STATE: Maryland COUNTRY: USA ZIP: 20877 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: LIM FC compatible OPERATING SYSTEM: PC-DDS/MS-DOS SOFTWARE: PACENTIN NUMBER: US/08/461,823 FILING DATE: 05-UN-1995 CLASSIFICATION NUMBER: US/08/461,823 FILING DATE: 05-UN-1995 CLASSIFICATION NUMBER: US/08/461,823 FILING DATE: 16-DEC-1993 PRIOR APPLICATION NUMBER: US/08/168,621 APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: US/08/168,621 APPLICATION DATA: APPLICATION D	7044
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US-09-762-195-2/c

; Sequence 2, Application US/09762195

; Patent No. 6677319

; GENERAL INFORMATION:
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US-09-023-655-1168/c
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APPLICANT: Stremmel, Wolfgang
                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (650) 845-41 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
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IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cocks,
APPLICANT: Susan
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                 1678
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CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                 CGAACCAGGGCACGTGCAATGGCGA 1654
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                                                                                                                                                                                                100.0%; Score 25; DB 4; Length 3924; ilarity 100.0%; Pred. No. 0.089; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.087;
Mismatches 0
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-762-195-2
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CURRENT APPLICATION NUMBER: US/09/762,195
CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP99702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
PRIOR PRIOR DATE: 1998-08-06
PRIOR FILING DATE: 1998-08-06
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 23
                GENERAL INFORMATION:
APPLICANT: STOCKER, PENNY J.
APPLICANT: STEIMEL-CRESPI, DO
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPR
FILE REFERENCE: G0307/7018
                                                                                                                                    Sequence 1, Application US/09672810 Patent No. 6617450
                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 4; Best Local Similarity 100.0%; Pred. No. 0.089;
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Patent No. 6677319
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: PCT/EP99702426
PRIOR FILING DATE: 1999-08-06
PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1998-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 198 57 570.8 DE PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stremmel, Wolfgang
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
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CURRENT APPLICATION NUMBER: US/09/672,810
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                                    P-GLYCOPROTEINS AND USES THEREOF
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Pred. No.
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CURRENT FILING DATE: 2000 PRIOR APPLICATION NUMBER:

2000-09-28 BER: US_60/156,921

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; LOCATION: (100)...(3940)
US-09-672-810-1
                                                                                                                                                                                                               RESULT 7
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; LOCATION: (100)...(3949)
US-09-672-810-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARR:
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                                                                                                                                                   Sequence 1, Application US/08784649A Patent No. 5830697
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Best Local Similarity 100.0%;
Matches 25; Conservative 0
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: G0307/7018
CURRENT APPLICATION NUMBER: US/09/672,810
CURRENT FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
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                                                 APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
                    NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                        1748 CGAACCAGGCACGTGCAATGGCGA 1724
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Fish & Richardson
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Pred. No. 0.
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RESULT 8
US-08-784-649A-5/c
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APPLICATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5, Application US/08784649A Patent No. 5830697
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APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT
TITLE OF INVENTION: CYCLOSPORIN MODULATION
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No.
REFERENCE/DOCKET NUMBER: 0603
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/784,649
                                                                                                                                                                                                                                                                        ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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STRANDEDNESS: BIL
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                                                                                                                                                                                                                                                                                                                                                                 CITY: Menlo Park
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les 25; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
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100.0%; Pred. No. 0.09;
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                                                                                                                                                                                                                        Version
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SEQUENCE CHARACTERISTICS:

MOLECULE TYPE:

TOPOLOGY:

linear

CDNA

STRANDEDNESS: single

nucleic acid

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US-08-181-471-2
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                                                                                                                                                                                                                                                                             TELEPHONE: 619-792-3680
TELEPAX: 619-792-9477
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4646 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loc
Matches
                                                     Matches
                                                                   Query Match
Best Local Similarity
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/041

FILING DATE: 02-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: ANTO

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-92-3680
                                                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDITION TYPED: 10 / 1011 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Li, Lingna
APPLICANT: Lishko, Valeryi K.
TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                OLECULE TYPE:
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                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 13-JAN CLASSIFICATION: 424
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nes 25; Conservative
                                                                                                                                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                       : YEOTOGO
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                                                   25;
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1 CGAACCAGGGCACGTGCAATGGCGA 25
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                                                                                                                                                                                                                                                                  nucleic acid
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12526 High Bluff Drive, Suite 300
                                                  100.0%; Score 25; DB 1 ilarity 100.0%; Pred. No. 0.09; Conservative 0; Mismatches
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                                                                                 DB 1; Length 4646;
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US-09-023-655-1167/c
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                                                                                                                                                              Sequence 18, Application US/08583276
Patent No. 5837536
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                GENERAL INFORMATION:
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APPLICANT: Nienhulb, APPLICANT: Tolstoshev, Paul
APPLICANT: Tolstoshev, Paul
TITLE OF INVENTION: MULTIDRUG RESISTANCE GENES AND IMPROVED
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
TITLE OF INVENTION: SELECTION OF CELLS TRANSDUCED WITH SUCH GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for 1
                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
LIBRARY: GENBANK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jeffrey TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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CLONE: 9187468
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CALIFORNIA
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                                                                                                                             McDonagh, Kevin T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (650) 855-0555
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Pred. No.
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

6 Becker Farm Road

Carella, Byrne, Bain, Gilfillan, Cecchi & Stewart

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US-08-752-447-1/c
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PILING DATE: 31-0CT-1994
APPLICATION NUMBER: 07/887
FILING DATE: 22-MAY-1992
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 4669 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08752447 Patent No. 5994088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: NO. 5994088nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE_JOOKET NUMBER: 95,1122
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6 CITY: ROSeland CITY: New Jersey 115A
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
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APPLICATION NUMBER: US/01
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Methods and Reagents for Preparing TITLE OF INVENTION: Using Immunoligeal Agents Specific NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: 3.5 inch diskette
                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Mechetner, APPLICANT: Roninson,
                                                                                                                                                                                                                                                                                      ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd STREET: 300 South Wacker Drive, Seventh Floor CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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Roninson, Igor B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 25; DB 2; Length 4669; 100.0%; Pred. No. 0.09;
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                       95,1121
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for P-glycoprotein
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RESULT 13
US-09-316-167-1/c
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Mechetner
APPLICANT: Roninson,
                                                                                                 TELEPHONE: 312-913-000
TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UMBER: 08/75:
APPLICATION UMBER: 08/75:
PILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: NO. 63.653.57nan, Kev-
REGISTRATION NUMBER: 35,3
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/316,167
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                    REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                 SEQUENCE CHARACTERISTICS LENGTH: 4669 base pai
MOLECULE TYPE: CDNA
               STRANDEDNESS:
TOPOLOGY: lir
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Local Similarity 100.0%;
Les 25; Conservative (
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STRANDEDNESS: single
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                                               TYPE: nucleic acid
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                                                                 4669 base pairs
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425..4264
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Methods and Reagents for Preparing and
Using Immunoligcal Agents Specific for P-glycoprotein
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Pred. No. 0.09;
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LOCATION:

1..424

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-09-316-167-1
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US-09-397-233-1/c
US-09-397-233-1/c
; Sequence 1, Application US/09397233
; Patent No. 6630327
; GENERAL INFORMATION:
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Best Local Similarity
Matches 25; Conserv
   Best Local Similarity Matches 25; Conserv
                                      Query Match
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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NAME: NO. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-199
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Mechetner, Eugene
Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunological Agents Specific for P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 95,1121-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
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COUNTRY: USA
                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                          NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4669 base pairs
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100.0%; Score 25; DB 4; Length 4669; ilarity 100.0%; Pred. No. 0.09; Conservative 0; Mismatches 0; Indels
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RESULT 15
5206352-3/c
;Patent No.
Search completed: February 9, 2005, 17:11:19 Job time : 79.592 secs
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                                                                                                                                                                                                          5206352-3
                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                              ; APPLICANT: Rominson, Igor B.;Pastan Ira H.;Gottesman,
                                                                                                                                                                                                                                         SEQ ID NO:3:
                                                                                                                                      Matches
                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/622,836
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                         LENGTH: 4669
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                                                                    2064 CGAÁCCAGGGCÁCGTGCAATGGCGA 2040
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                                                                                                                                   100.0%; Score 25; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 18 25 100.0 3860 6 ABA94366 A	18 25 100.0 3860 6 ABA94366 P		17 25 100.0 3860 6 ABA94365	16 25 100.0 3860 3 AAZ49333	15 25 100.0 3860 3 AAZ49332	14 25 100.0 3858 12 ADH22599	13 25 100.0 3852 8 ABT14496	12 25 100.0 3843 6 ABQ78185 F	100.0 3840 6 ABL91687	100.0 3840 6 ABX09965	9 25 100.0 3840 6 ABZ35722	100.0 3840 6 ABV78146	7 25 100.0 3837 12 ADH22602	6 25 100.0 2726 2 AAT43322	5 25 100.0 2726 2 AAQ70916	100.0 2726 2 AAQ70907	100.0 2307 6 ABS65230	100.0 25 6 AAD39003	100.0 25 6 AAD39013	NO. Score Match Length DB ID D	
	Aaz94742 Human ATP	Aba94366 Human BCR	Duman	Aaz49333 Human G18			Abt14496 knesus mo	Abq78185 Human MDR		Human	Human	Human	2 CDNA	Aat43322 Multidrug	Aaq70916 Multidrug			Aad39003 Human mdr		Description	

		c 43		c 41		w	c 38			ω	C 34	c 33	c 32	c 31		N	c 28	N	c 26		c 24		c 22	c 21
25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	-	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	100	25 100.0	25 100.0	25 100.0	25 100.0	25 100.0	
4646	4646	4646	4646	4646	4643	4643		4643	4643	4643		-	4378	4349	4264	4264	4195	4186		4043	4039	3988		3924
6 AAD38994	6 ABL68880	6 ABL68592	3 AAZ94738	2 AAQ72872	13 ADP54881		12 ADP18689	10 ABX77217	6 ABV74349	6 ABV94267	6 ABS76368	6 ABS65229	2 AAQ04522	4 AAH57442	2 AAV66534	2 AAV66533	4 AAF86128	4 AAF86127	13 ACN41835	13 ACN41836	13 ACN43502	3 AAZ88973	11 ADI31842	6 ABN95801
Aad38994 Human mar					_	Human	Human		Human			CUNA				Mutated			U			a	Ad131842 Human CUN	Abn95801 Gene #229

ALIGNMENTS

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RESULT 1
AAD39013/c
ID AAD390
Human mdr1 gene HIF-1 binding site DNA #6.
                                                                                                                                       AAD39013 standard;
                                                                                                                          23-SEP-2002
                                                                                                                                 AAD39013;
                                                                         misc_binding
                                                                                    Homo sapiens
                                                                                                                          (first entry)
                                                                          Location/Qualifiers
                                                                                                                                        DNA;
                                                                                                                                        25
                                                                                                                                        BP.
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Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hyppoxia inducible factor-1; small ubiquitin-1!ke-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; ds.

02-MAY-2002. WO200234291-A2 /bound_moiety= "HIF-1"

26-OCT-2000; 2000US-0243542P. (BGHM) BRIGHAM & WOMENS HOSPITAL INC.

25-OCT-2001; 2001WO-US049856

Colgan SP;

WPI; 2002-471427/50.

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1 binding molecules.

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Best Local
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Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small ubiquitin-like-modifier-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-1ike-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; antisense; phosphorothioate backbone; ss.
                                                                                                        WPI; 2002-471427/50
                                                                                                                                                                                                                                                          26-OCT-2000; 2000US-0243542P
                                                                                                                                                                                                                                                                                                         25-OCT-2001; 2001WO-US049856
                                                                                                                                                                                                                                                                                                                                                             02-MAY-2002
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                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Phosphorothioate backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               base= OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 25; DB 6;
Pred. No. 0.084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 3
ABS65230/c
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        element (HRE) binding molecules or antisense nucleic acid molecules and sumo-1 binding molecules or antisense molecules are useful for treating subject having or at risk of developing haematologic malignancy or MDE (e.g. a lymphoid disorder or a myeloid disorder). The lymphoid disorders include lymphocytic leukaemia or chronic lymphoproliferative disorders e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia, e.g. angiogenic myeloid metaplasia, essential thrombocythaemia roblycythaemia vera. This invention is used in gene therapy. The present sequence is an antisense oligo targetted to HRE in the mdr1 gene (mdr1-HRE) to inhibit its expression. This oligo is used in the exemplification of the invention
                      Novel nucleic acid sequence, tumor involved genes, useful cancer, for evaluating cancer
                                                                                                                                                                                                                                                                                                                                                                                                       numan; ss; gene; splice variant; tumour-involved gene; pharmaceutical composition; cancer; diagnostic; tumour; endothelial cell; cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA encoding tumour involved gene (TIG) splice variant, NV-31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                 WPI; 2002-635679/68
                                                                                                                                                                                                                                                                             13-MAR-2001; 2001US-00805020
                                                                                                                                                                                                                                                                                                          04-JUL-2002
                                                                                                                                                                                                                                                                                                                                       US2002086384-A1
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                 14-MAR-2000;
16-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding molecules or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e invention relates to a method of treating a subject having or at I developing a haematologic malignancy or multidrug resistance (MDR) e method involves administering hypoxia inducible factor-1 (HIF-1) rding molecules or small ubiquitin-like-modifier (SUMO)-1 binding lecules or hIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive lecules or HIF-1-SUMO-1 complex modulators. mdr1-hypoxia responsive
                                                                                                                                                                                                                                                                                                                                                                                            therapy.
                                                                                                                              2
                                                                                                                                                                          LEVINE Z.
DAVID A.
ROMANO C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                           BERNSTEIN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAACCAGGGCACGTGCAATGGCGA
                                                                                                                            David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; llarity 100.0%; Conservative 0
                                                                                                                                                                                                                                  2000IL-00135402
2000IL-00136154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                               Romano
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G; 2 T; 0 U; 0 Other;
                      which is an alternative splicing variant for detecting cancer, predisposition to state and in gene therapy for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                               Bernstein
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No.
                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic; tumour; gene therapy;
ion; cell proliferation; apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TIG;
                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis;
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Enzymatic amplification of target nucleic acid sequences detect a mutation or allele in the target, e.g. that caus
      nces in
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144 CGAACCAGGGCACGTGCAATGGCGA 120

RESULT 4
AAQ70907/c
ID AAQ7099
XX
AAQ7099
AC AAQ709
AC AAQ709
AC AAQ709
AC AAQ709
XX
AC AAQ709
XX
DT 25-MAR
DT 27-MAR
XX
Multid
Mul 용 The invention discloses isolated human nucleic acid alternative splicing CC variants that are all tumour-involved genes (TIGs). The nucleic acids and CC polypeptides are useful for determining the level of a nucleic acid or CC polypeptide in a biological sample, for detecting a variant nucleic acid or polypeptide in a biological sample, for detecting a variant nucleic acid or polypeptide sequence in a biological sample, for determining the level of variant nucleic acid or polypeptide sequences in a biological sample cC and for determining the level of the variant sequence in a first biological sample and the level of the original sequence in a cC the variant has been varied by alternative splicing in a second composition comprising a carrier and the nucleic acid, is useful for treating diseases (e.g. cancer) that can be ameliorated or cured by increasing or decreasing the level of the encoded protein. The nucleic acids are also useful for diagnostic purposes, especially for detecting cancer or a predisposition to cancer, for evaluating the state or cc aggressiveness of cancer disease, in basic research, for understanding the physiological function of the original TIG, in targeting or cc cycle of the same type of cells which may be helpful for the development of pharmaceuticals for various cancer stages in which cell cycle is non-normal, for determining mutations in tumour-involved genes and in gene composition to the variant product and modulating its activity and for compounds capable of binding to the variant product and modulating its activity and for composition to cancer stages in which cell cycle is non-composition. The sequences presented in composition as well as to composite either ex vivo or in vivo. The sequences presented in composition and disclosed or in vivo. The sequences presented in composition and disclosed in the TIGs disclosed Matches Query Match Sequence 2307 Claim 1; Multidrug-resistance 25-MAR-2003 27-MAR-1995 AAQ70907 standard; Multidrug-resistance; MDR-1 gene; AAQ70907; 04-AUG-1994. WO9417206-A1 Synthetic WPI; 1994-264118/32. Bhatnagar SK, 12-NOV-1993; Local 2064 ... 25; ONCOR Similarity Page 60-61; 180pp; English CGAACCAGGGCACGTGCAATGGCGA 25 CGAACCAGGGCACGTGCAATGGCGA Conservative (revised) (first en BP; 662 A; 441 George 93US-00010433 93WO-US010883 DNA; entry) 100.0%; gene MDR-1 AL; 2726 <u>,</u> ВP C; 591 G; Score 25; Pred. No. 0 Mismatches 612 T; 0 U; 1 Other; 0.14; DB 6; Length 2307; 0 Indels ٥, mixt. -Gaps ç 0

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AAQ70916/c
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Best Local S
Matches 25
                       Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This gene is used as an example of a rarger was a mixture using various DNA amplification of nucleic acid sequences in a mixture using various DNA probes/primers. The method may be used to detect a mutation or allele probes/primers that that causes a genetic disease: (Updated on 25-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2726 BP; 818 A; 538 C; 642 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ70916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 30; 50pp; English.
                                                                                      This gene is used as an example of a target DNA in a method for the amplification of nucleic acid sequences in a mixture using various DNA probes/primers. The method may be used to detect a mutation or allele the target, e.g. that that causes a genetic disease. (Updated on 25-MA 2003 to correct PN field.)
                                                                                                                                                                             Enzymatic amplification of target nucleic acid sequences to form exact modified copies - has increased fidelity and can identify point mutatic or allele(s).
                                                                                                                                                                                                                                                                                              27-JAN-1993;
16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                     04-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                       Multidrug-resistance; MDR-1 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Multidrug-resistance gene MDR-1.
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27-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAQ70916;
                                                                                                                                                        Disclosure; Page 30; 69pp; English.
                                                                                                                                                                                                                             WPI; 1994-264122/32.
                                                                                                                                                                                                                                                  Bhatnagar SK,
                                                                                                                                                                                                                                                                                                                                25-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                             WO9417210-A1
                                                                  Sequence
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                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAACCAGGCACGTGCAATGGCGA
                                                                   2726
  CGAACCAGGGCACGTGCAATGGCGA 25
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                        Conservative
                                                                  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
                                                                                                                                                                                                                                                                         INC.
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93US-00168621.
                                                                                                                                                                                                                                                  George
                                                                                                                                                                                                                                                                                                                                94WO-US000748
                                                                   818 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
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                                   100.0%;
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                                                                   538 C; 642 G;
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                        0;
                                 Score 25;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25;
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                         Mismatches
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                                                                     728 T; 0 U; 0 Other;
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                                                BB
                                    .14;
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                                             Length 2726;
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                          Indels
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                          Gaps
                                                                                                     llele in
25-MAR-
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ARESULT 6
AAT43322/c
ID AAT433
XX PCR; p
XX PCR; p
XX LCR; h
XX LCR; h
XX PCR; p
XX LCR; h
XX LCR; p
XX LCR; h
XX LCR; h
XX LCR; p
XX LCR; p
XX AMP163
PF 04-UN
PR 05-UN
PR 06-UN
PR 06-UN
PR 06-UN
PR 06-UN
PR 07-UN
RESULT 7
ADH22602/c
ID ADH22602 s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents the multidrug resistance gene (MDR-1) amplified CC by the primers shown in AAT43320 and AAT43321. This sequence can be used CC as a target in the method of the invention, for enzymatically amplifying CC atarget nucleic acid (TNA) sequence contained in a nucleic acid or comparises. The method comprises using three primers, one complementary CC polymerase. The method comprises using three primers, one complementary to a first segment of the TNA, a second complementary to a second segment to the first primer, and a third which is comparise on the first primer. The first two primers are hybridised to the TNA, and a fused amplification product is created from the TNA using CC the third primer. The fused product is dissociated, and hybridised to the third primer, which is then extended. The extended modified CC amplification product is hybridised to the first two primers, and these CC two primers are ligated. Each of the primers may be labelled using a CC different label so that the method can be used to detect the presence of CC amutation or allele by detecting whether the labelled primer is CC contained within the fused amplification product or the extended contained within the fused amplification product or the extended CC amplification product. The method of the invention combines certain CC extended, and the fact that the entire TNA sequence does not need or the known.
                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amplification method avoiding the detection of mutation(s) a
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human; multidrug
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                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                        CGAACCAGGGCACGTGCAATGGCGA 25
                                                                                                                                                 CGAACCAGGGCACGTGCAATGGCGA 120
                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-00461823
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                                                                                                                                                                                                                                                                                                                                                                              818 A; 538 C; 642 G;
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resistance
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                                                                                                                                                                                                                                                                                            Score 25;
Pred. No.
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                                                                                                                                                                                                                                                                 Mismatches
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gene; MDR-1; ds.
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                                                                                                                                                                                                                                                                                            0.14;
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standard; cDNA; 3837

밁 S

Query Match Best Local Matches

25; Similarity

100.0%; ilarity 100.0%; Conservative

٥, Score Pred.

Mismatches 25

25; No.

0.14;

DB 12; 0

Length 3837; Indels

0

Gaps

0

CGAACCAGGGCACGTGCAATGGCGA

Sequence

3837

BP; 1130 A;

772 C; 962 G;

973 T; 0 U; 0 Other;

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This invention relates to novel isolated polynucleotides identified as CC human transporters and ion channels (TRICH), and the encoded polypeptides CC thereof. Specifically, it describes using these TRICH molecules, as well as agonists, antisponists, antibodies, expression vectors and host cells, in appropriate screening and toxicity assays to assess the effects of CC exogenous compounds on TRICH expression. The present invention describes CTRICH compositions that are useful in the diagnosis, treatment and CC prevention of various disorders such as cell proliferative (e.g. arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma), CC arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma), CC explored (e.g. epilepsy, stroke) and developmental (e.g. Cushing's syndrome hypothyroidism) and for infections. Accordingly, these TRICH collecties can be used for gene therapy purposes and exhibit various activities such as cytostatic, antiinflammatory, immunosuppressive, CC antiasthmatic, anticonvulsant, nootropic and neuroprotective.

CC protein interactions, drug-target interactions and gene expression profiles. This polynuclectide sequence is a human TRICH cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baughn MR, Because T., H
Emerling BM, Griffin JA, H
Jin P, Kable AE, Khare R,
Pichardson TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human transporters and ion channels (TRICH), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant TRICH expression e.g. cancer, AIDS, atherosclerosis, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-2002; 2002US-0377445P.
03-MAY-2002; 2002US-0377444P.
05-JUN-2002; 2002US-0386497P.
11-JUN-2002; 2002US-0388180P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arteriosclerosis; cancer; autoimmune/inflammatory; AIDS; asthma;
neurological; epilepsy; stroke; developmental; Cushing's syndrome;
hypothyroidism; infection; gene therapy; cytostatic; antiinflammatory;
immunosuppressive; antiasthmatic; anticonvulsant; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 12; SEQ ID NO 100; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ADH22536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ss; human; transporters and ion channel; TRICH; cell proliferative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA encoding a human transporter & ion channel (TRICH) protein SeqID100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bulloch SA, Chang H, Elliott VS;
JA, Hafalia AJA, Ison CH, Jackson AA, Jian
re R, Lee SV, Lee S, Mason PM, Marquis JP;
n TW, Swarnakar A, Tran UK, Chawla NK;
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RESULT 9
ABZ35722/c
ID ABZ35722 8
XX
AC ABZ35722;
XX
DT 07-FEB-200
.XX
DE Human mdr-
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ABV78146/c
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                                                                                                                                                                                                            Query Match
Best Local S
Matches 25
                                                                                                                                                                                                                                                                                                        The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNAI) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (asl) of dsRNAI is complementary to (I) and at least one end of dsRNAI has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting expression of target gene, useful e.g. for inhibiting oncogenes, by administering double-stranded RNA complementary to target and having an overhang.
  Human mdr-1
                                                                                                                                                                                                                                                                    Sequence 3840 BP; 1130 A; 738 C; 957 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-590671/63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kreutzer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-2001; 2001DE-01000586.
26-0CT-2001; 2001DE-01055380.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JAN-2002; 2002WO-EP000152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virucide; protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA inhibition; dsRNA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mdr-1 DNA SEQ ID NO 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2002
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                              07-FEB-2003
                                                                                                                                                      1637
                                                                                                                                                                                                                                                                                                 related to the invention
                                                                                                                                                                                                               25;
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                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                        CGAACCAGGGCACGTGCAATGGCGA 25
                                                                                   etandard;
                                                                                                                                                        CGAACCAGGGCACGTGCAATGGCGA 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 131-132; 203pp; German.
 polynucleotide SEQ ID
                                                                                                                                                                                                            100.0%; Score 25; Dilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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                              (first
                                                                                   DNA; 3840
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                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene expression inhibitor; oncogene; cytostatic;
gene; ds.
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                                                                                                                                                                                                                                                                     1015
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                                                                                                                                                                                                               0
                                                                                                                                                                                                                                        Length 3840;
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21-NOV-2002

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RESULT 10
ABX09965/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Sim
Matches. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Double stranded RNA; dsRNA; RNA; RNA inhibition; cytostatic; virucide; protozoacide; gene expression; antisense; tumour; infection; Plasmodium; virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus; Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Inhibiting expression of target genes, useful e.g. for treating tumors, by introducing into cells two double-stranded RNAs that are complementary to the target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-683450/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3840
                                                                                                                                      Oligoribonucleotide; interferon; oncogene; cytokine;
                                                                                                                                                                                             Human
                                                                                                                                                                                                                                                     23-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                 ABX09965 standard; DNA; 3840
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DE10100587-C1
                                                                                                         prion; inhibition;
                                                                                                                                                                                                                                                                                                            ABX09965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Page 27-28; 100pp; German.
                                                                                                                                                                                             mdr-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGAACCAGGGCACGTGCAATGGCGA 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAACCAGGGCACGTGCAATGGCGA 25
                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 6 ilarity 100.0%; Pred. No. 0.14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                             fragment SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        738 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 3840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                            Id;
                                                                                                                                            developmental;
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RESULT 11
ABL91687/c
ID ABL91687 standard; DNA; 3840
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or virolds (pathogenic in humans, animals or plants). Treating the cells with interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention
               WPI; 2002-270454/32
                                           Kreutzer R,
                                                                                                   09-JAN-2001; 2001DE-01000586
                                                                                                                                 09-JAN-2001; 2001DE-01000586
                                                                                                                                                               11-APR-2002.
                                                                                                                                                                                            DE10100586-C1.
                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                     cytostatic; virucide; protozoacide; antibacterial;
                                                                                                                                                                                                                                                                   Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen; Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                               28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                           ABL91687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3840 BP; 1130 A; 738 C; 957 G; 1015 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inhibiting expression of target genes, e.g. oncogenes, in cells, by introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JAN-2001; 2001DE-01000587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-JAN-2001; 2001DE-01000587
                                                                      (RIBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 32-33; 98pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-742209/81.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel method for inhibiting expression of a sarget gene by introducing into the cell that contains the target gene at least one oligoribonucleotide (dsRNAI) that has a double-stranded (ds)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1637
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                                                                       RIBOPHARMA AG
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ilarity 100.0%;
Conservative C
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Pred. No. 0.
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                                        Hadwiger P;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least one end a single-stranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tumours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
                                                                                                                                                                  31-JAN-2001; 2001JP-00024723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ78185 standard; cDNA; 3843
                       Disclosure; Page 6-11; 14pp; Japanese.
                                                    primer
                                                                Presuming the side effect
                                                                                             P-PSDB; ABB83950
                                                                                                          WPI; 2002-639348/69
                                                                                                                                                                                              31-JAN-2001; 2001JP-00024723.
                                                                                                                                                                                                                                                   JP2002223769-A.
                                                                                                                                                                                                                                                                                                          variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human MDR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABQ78185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3840 BP; 1130 A; 738 C; 957 G;
                                                                                                                                                                                                                          13-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminal bases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting gene expression in cells, useful for e.g. treating tumors, introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                      (SRLS-) SRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1637 CGAACCAGGGCACGTGCAATGGCGA 1613
                                                      set.
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                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressant; tacrolimus; cyclosporin; MDR1; SNP;
nucleotide polymorphism; gene; ss.
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/*tag= b
                                                                                                                                                                                                                                                                                                                        /product= "MDR1"
                                                                                                                                                                                                                                                                             standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
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                                                                 of an
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Pred. No.
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                                                                 immunosuppressant
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The invention relates to presumption of the side effect of at least one

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Matches 25
                                                                                                         Query Match
Best Local S
Matches 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhesus monkey; 
P-glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhesus monkey P-glycoprotein coding sequence.
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                                                                                                                                                                                                                                                                     The invention comprises the amino acid and coding sequence of a rhesus monkey (Macaca mulatta) P-glycoprotein and related P-glycoproteins. The DNA and protein sequences of the invention are useful in assays for evaluating the bioavailability of drugs, as well as the optimisation or discovery of drugs for the treatment of disease associated with P-glycoprotein transporter activity. The present cDNA sequence encodes the Rhesus monkey P-glycoprotein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a P-glycoprotein of monkey, useful in assays for evaluating bioavailability of as for the optimization or discovery of drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-2001; 2001US-0277095P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-2002; 2002WO-US008325
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                                                                                                                                                                                                            Sequence 3852 BP; 1123 A; 750 C; 967 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Page 51-56; 103pp; English.
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                                  CGAACCAGGGCACGTGCAATGGCGA 25
  CGAACCAGGGCACGTGCAATGGCGA 1625
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SR;
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                                                                                                                                        Score 25;
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                                                                            This invention relates to novel isolated polynucleotides identified as CC human transporters and ion channels (TRICH), and the encoded polypeptides CC thereof. Specifically, it describes using these TRICH molecules, as well CC as agonists, antagonists, antibodies, expression vectors and host cells, in appropriate screening and toxicity assays to assess the effects of CC exogenous compounds on TRICH expression. The present invention describes TRICH compositions that are useful in the diagnosis, treatment and CC prevention of various disorders such as cell proliferative (e.g. arteriosclerosis, cancer), autoimmune/inflammatory (e.g. AIDS, asthma), CC entrological (e.g. epilepsy, stroke) and developmental (e.g. Cushing's molecules can be used for gene therapy purposes and exhibit various activities such as cytostatic, antiinflammatory, immunosuppressive, CC antiasthmatic, anticonvulsant, nootropic and neuroprotective.

CC Purthermore, a microarray is useful in monitoring or measuring protein-creative anticons, drug-target interactions and gene expression profiles. This polynucleotide sequence is a human TRICH cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-2002;
03-MAY-2002;
05-JUN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA encoding a human transporter & ion channel (TRICH) protein SeqID97.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human transporters and ion channels (TRICH), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant TRICH expression e.g. cancer, AIDS, atherosclerosis, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-MAY-2003; 2003WO-US014026
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P-PSDB; ADH22533.
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Kable AE, Khare R,
ar J, Richardson TW,
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; 2002US-0386497P.
; 2002US-0388180P.
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, Lee SY, Lee S, Ma
, Swarnakar A, Tran
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AJA, Ison CH, Jackson
, Lee S, Mason PM, Ma
kar A, Tran UK, Chawla
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Chawla NK;
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Matches Best Local Query Match

Similarity

100.0%; Score 25; 100.0%; Pred. No.

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(AXYSB187) where the Gly at position 185 is replaced by Val. The CC (ANYSB187) where the Gly at position 185 is replaced by Val. The CC invention relates to transducing haematopoietic stem cells with nucleic acid encoding an MDR protein and culturing the modified cells. The CC modified haematopoietic stem cells are useful in bone marrow transplantation (to reconstitute haematopoietic systems in patients who have undergone chemotherapy or radiation therapy) and in ex vivo gene therapy of genetic defects in cells derived from haematopoietic stem cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or leukaemia. The modified cells can also be used to identify factors involved in regulating proliferation and differentianion in haematopoietic stem cells. Haematopoietic stem cells that express MDR-1 while the patient is undergoing chemotherapy. Expansion of (rare) haematopoietic stem cells provides sufficient cells to permit standard biochemical analysis. Overexpression of MDR-1 allows cytokine-driven
                                                                                                                                                                                                                                                                                               This sequence represents cDNA encoding human wild-type multidrug resistance protein MDR-1. MDR-1 is a transmembrane efflux pump, responsible for the export of drugs from cells, particularly cancer cells. Wild-type MDR-1 shows increased resistance to etoposide and decreased resistance to vinca alkaloids compared with a mutant form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multidrug resistance; MDR-1; P-glycoprotein; transmembrane efflux pump; haematopoietic stem cell; transduction; bone marrow transplantation; chemotherapy; radiation therapy; cancer; gene therapy; gene replacement genetic defect; thalassaemia; Gauchier's disease; sickle cell anaemia; leukaemia; ex vivo expansion; cytokine; wild-type; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 68-70; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ex vivo expansion of hematopoietic stem cells transduced with a sequence encoding human multidrug resistance-1, used for bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human wild-type multidrug resistance-1 (MDR-1) cDNA.
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/note= "cDNA sequence of G185V human mutant MDR-1 given
in AAZ49333"
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/product= "Human wild-type MDR-1 protein"
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                                          Matches
                                                      Query Match
Best Local
                                                                                    Sequence 3860 BP; 1135 A; 746 C; 957 G;
                                                                                                        expansion of haematopoietic stem cells by at least 10-fold compared with a maximum of 4-fold in known procedures
1640
                                          25;
                    1 CGAACCAGGGCACGTGCAATGGCGA 25
                                                     Similarity
CGAACCAGGGCACGTGCAATGGCGA
                                          Conservative
                                                    100.0%;
                                         0; Mismatches
                                                     Score 25;
Pred. No.
1616
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                                                               Length 3860;
                                                                                     0 U; 0 Other;
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Search completed: February 9, 2005, 16:05:59
Job time: 246.69 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Published Applications NA:*

1: /cgn2=6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2=6/ptodata/1/pubpna/US06 NEW PUB.seq:*

3: /cgn2=6/ptodata/1/pubpna/US06 NEW PUB.seq:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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539.601 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIE

0 0 0 0 0 0 0 0 0 0 0	Result No.
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1000.0 1000.0 1000.0 1000.0	Query Match
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9 US-09-805-020-31 17 US-10-363-112-48 18 US-10-384-339C-30 15 US-10-101-433A-1 9 US-09-866-866A-3 9 US-09-866-866A-3 9 US-09-886-107-2299 17 US-10-641-643-1168 17 US-10-619-359A-1 17 US-10-619-359A-3 9 US-09-805-020-30	ID
Sequence 31, Appl Sequence 48, Appl Sequence 10, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2299, Ap Sequence 1168, Ap Sequence 1168, Ap Sequence 13, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	Description

RESULT 2 US-10-363-112-48/c ; Sequence 48, Application US/10363112

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Sequence 15, Appi	16,	e 244	Id, Api	Sequence 29889, A	2 6	Sequence 1	Sequence 4, Appli	4.	Sequence 59, Appl	414	33184,	/, Appii			Sequence 32, Appr	Sequence 1484, Ap	Sequence 265, App	Sequence 1424, Ap	5, App	5	, -			-	Sequence 1, Appli			. E		4 1	258,	1, Ap	'n

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Sequence 30, Application US/10384339C
Publication No. US20040175703A1
GENERAL INFORMATION:
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; LOCATION: (1)..(3825)
US-10-363-112-48
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PRIOR PILING DATE: 2002-01-09
PRIOR PPLICATION NUMBER: DE 10100586.5
PRIOR PILING DATE: 2001-01-09
PRIOR PILING DATE: 2001-10-09
PRIOR REPLICATION NUMBER: DE 10155280.7
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR PILING DATE: 2001-11-29
PRIOR PILING DATE: 2001-12-07
NUMBER: DE 10160151.4
PRIOR PILING DATE: 2001-12-07
NUMBER: DE 10160151.4
PRIOR PILING DATE: 2001-12-07
NUMBER: DE 500 ID. NOS: 173
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Matches 25
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                                                                                                                                                               TITLE: mdr-1
PATENT DOCUMENT NUMBER: AF016535
-10-384-339C-30
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                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET
FILE REFERENCE: 20200/2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 007643-0302189
CURRENT APPLICATION NUMBER: US/10/363,112
CURRENT FILING DATE: 2003-11-03
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/384,339C CURRENT FILING DATE: 2003-03-07
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NUMBER OF SEQ ID NOS: 62
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PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 60/229,663
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TITLE OF INVENTION: MODIFIED PROTEINS, ISOLATED NOVEL PEPTIDES, AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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ORGANISM: Homo sapiens
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CGAACCAGGGCACGTGCAATGGCGA 1613
                                      CGAACCAGGGCACGTGCAATGGCGA 25
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                                                                               Conservative
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                                                                                                100.0%; Score 25; DB 18
100.0%; Pred. No. 0.035;
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Pred. No. 0.035;
Mismatches 0;
                                                                             Mismatches
                                                                                                                    DB 18; Length 3840;
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; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 3860
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-866A-1
  밁
                                                                                                                                                                                                                                                                                                             PILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: PCT/US99/11825
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR PILING DATE: 1998-05-28
PRIOR FILING DATE: 1998-05-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                           PATEUR NO. 10-1
GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
PTIER REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/10101433A Publication No. US20030119726A1 GENERAL INFORMATION:
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                                                                                   Matches
                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09866866A Patent No. US20020102244A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hanscom, Sara
APPLICANT: Crespi, Charles
APPLICANT: Crespi, Charles
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307/70019
FILE REFERENCE: G00307/70019
CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/277,095
PRIOR APPLICATION NUMBER: US 60/277,095
PRIOR FILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Macaca mulatta
FEATURE:
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LOCATION: (1)..(3852)
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                                                                                                       Local
1640 CGAACCAGGGCACGTGCAATGGCGA 1616
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25; Conserv
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                                   CGAACCAGGGCACGTGCAATGGCGA 25
                                                                                 100.0%; Score 25; DB 9; ilarity 100.0%; Pred. No. 0.035; Conservative 0; Mismatches
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100.0%; Pred. No.
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                                                                                                                           Length 3860;
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US-09-866-866A-3/c
Sequence 3, Application US/09866866A
Patent No. US20020102244A1
GENERAL INFORMATION:

APPLICANT: Sorrentino, Brian

RESULT 6

GENE EXPRESSION

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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
FIGURIT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REPERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILLING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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                                                                                                                                                      RESULT 8
US-10-641-643-1168/c
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LENGTH: 3860
                                                                                    Sequence 1168, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2299
LENGTH: 3924
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Patent No. US20020142981A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells FILE REFERENCE: 1340-1-021CIP2
CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR PILIOR DATE: 1090-05-27
PRIOR APPLICATION NUMBER: 07/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR APPLICATION NUMBER: 60/086,988
                                                                                                                                                                                                                                                                                                                                                                        Query Match
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APPLICANT: Vockley
APPLICANT: Scherf,
APPLICANT: Gene Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: homo mapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Genbank Accession No. US20020142981A1 M23234
                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1640 CGAACCAGGCACGTGCAATGGCGA 1616
                                                                                                                                                                                                                                             1678
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGAACCAGGGCACGTGCAATGGCGA 25
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                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 9; Length 3924; 100.0%; Pred. No. 0.035; tive 0; Mismatches 0; Indels
                                                                    Benjamin G.
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RESULT 9
US-10-619-359A-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                        SEQ ID NO
                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR PPLICATION NUMBER: US 60/158,818
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR APPLICATION NUMBER: US 09/672,810
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                     FILE REFERENCE: G00307.70020.US
CURRENT APPLICATION NUMBER: US/10/619,359A
CURRENT FILING DATE: 2003-07-14
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
                                                                                       SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STOCKER, PENNY J.
                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1168: SEQUENCE CHARACTERISTICS:
ORGANISM: Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/10/641,643
PILING DATE: 14-Aug-2003
PILING DATE: 14-Aug-2003
CLASSIFICATION NUMBER: CUnknown>
PRIOR APPLICATION NUMBER: <Unknown>
PILING DATE: CUnknown>
APPLICATION NUMBER: CUNKnown>
PILING DATE: CUNKnown>
PILING DATE: CUNKnown>
APPLICATION NUMBER: 37,071
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1168:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1678 CGAACCAGGGCACGTGCAATGGCGA 1654
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                                            4186
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STATE: CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 3924 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENBANK
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US-09-805-020-30/c
; Sequence 30, Application US/09805020
; Publication No. US20020086384A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, Zurit
; TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
; FILE REFERENCE: 2786-0168P
; CURRENT APPLICATION UNMER: US/09/805,020
; CURRENT FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(4533)
OTHER INFORMATION: any n = a,
US-09-805-020-30
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Best Local S
Matches 25
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Best Local S
Matches 25
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                                                                                                                                                            SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: PENNY J. APPLICANT: STOCKER, PENNY J. APPLICANT: STEIMEL-CRESPI, I APPLICANT: CRESPI, CHARLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/156,921
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/158,818
PRIOR FILING DATE: 1999-10-12
PRIOR PPLICATION NUMBER: US 09/672,810
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: STEIMEL-CRESPI, DOROTHY T.
APPLICANT: CRESPI, CHARLES L.
TITLE OF INVENTION: P-GLYCOPROTEINS AND USES THEREOF
FILE REFERENCE: G00307,70020.US
CURRENT APPLICATION NUMBER: US/10/619,359A
CURRENT FILING DATE: 2003-07-14
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LOCATION: (100)...(3949)
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                                                                                                                                      ENGTH: 4533
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nes 25; Conserv
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25; Conservative
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100.0%; Pred. No. 0.035;
ative 0; Mismatches
                    a,c,g,t any unknown or other
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Pred. No. 0.035;
; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-072-621-2
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US-10-072-621-2/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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Best Local
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Best Local Similarity
          TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification, TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer FILE REPERENCE: URI-030 CURRENT FILING DATE: 2002-03-14 PRIOR APPLICATION NUMBER: 60/276,025 PRIOR FILING DATE: 2001-03-14 PRIOR FILING DATE: 2001-03-14 PRIOR APPLICATION NUMBER: 60/276,025 PRIOR APPLICATION NUMBER: 60/25,149 PRIOR APPLICATION NUMBER: 60/276,026 PRIOR FILING DATE: 2001-09-26 PRIOR FILING DATE: 2001-03-14 PRIOR APPLICATION NUMBER: 60/276,026 PRIOR FILING DATE: 2001-03-14 PRIOR FILING DATE: 2001-03-14 PRIOR APPLICATION NUMBER: 60/276,026 PRIOR FILING DATE: 2001-03-14
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NUMBER OF SEQ ID NOS: 10
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APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: POLIARD, Michalle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR ACTIVITY
FILE REFERENCE: 100103.402
CURRENT APPLICATION NUMBER: US/10/072,621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: John MONAHAN
APPLICANT: Manjula GANI
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APPLICATION NUMBER: 60/324,967
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Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
Rachel E. MEYERS
Michael MORRISEY
Peter CLANDT
                                                                                                                                                                                                                                      Xumei ZHAO
Karen GLATT
                                                                                                                                                                                                                                                                                                              Gordon B. MILLS
Robert C. BAST, Jr.
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                                                                                                                                                                                                                                                                                                    Karen LU
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Pred. No.
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LENGTH: 4643
TYPE: DNA
CORGANISM: Homo sapiens
US-10-097-340-1
RESULT 15
US-09-968-007A-459/c
US-09-968-007A Application US/09968007A
; Sequence 459, Application US20040115625A1
; Publication No. US20040115625A1
; GENERAL INFORMATION:
GENERAL INFORMATION: Gene Determination and Therapeutic Screening Usining Signal TITLE OF INVENTION: Gene Sets
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION UMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , OTHER INFORMATION: atp-binding cassette, sub-family b , OTHER INFORMATION: (mdr/tap), member 1 (ABCB1) gene. US-10-007-926A-258
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US-10-007-926A-258/c
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LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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PRIOR APPLICATION NUMBER: 60/311,732
PRIOR TILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
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Best Local Similarity 100.0%; Pred. No. 0.035;
Matches 25; Conservative 0; Mismatches
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Best Local Similarity
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APPLICANT: NGUYEN, CATHERINE
APPLICANT: VIENS, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
FILE REPERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver: 2.1
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BIRNBAUM, DANIEL
NGUYEN, CATHERINE
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Pred. No. 0.035;
Mismatches
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PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR PILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR PELLING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,316
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
SOFTWARE: Patentin version 3.0
SEQ ID NO 459
LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
US-09-968-007A-459
Search completed: February Job time: 268.667 secs
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Best Local
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Local Similarity 100.0%; Pred. No. 0.035;
hes 25; Conservative 0; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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nucleic search, using
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1: gr
2: r
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ALIGNMENTS

JOURNAL MEDLINE PUBMED COMMENT REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 F07318 LOCUS DEFINITION FEATURES TITLE source Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 290) 1 (bases 1 to 290) 2 (bases 1 to 290) 3 (bases 1 to 290) 4 (bases 2 to 290) 5 (bases 2 to 290) 5 (bases 3 to 290) 6 (bases 3 to 290) 7 (bases 4 to 290) 7 (bases 4 to 290) 7 (bases 5 to 290) 7 (bases 6 to 290) 7 (bases 6 to 290) 7 (bases 7 to 290) 7 (bases 7 to 290) 7 (bases 7 to 290) 7 (bases 1 to 290) 7 (bases 1 to 290) 7 (bases 1 to 290) 7 (bases 7 to 290) 7 (bases 1 to 290 Genethon Centre de recherch 1, rue de l'Internationale, Tel: 33169472800 Fax: 33160778698 F07318 290 bp mRNA linear EST 20-FEB HSC22A071 normalized infant brain cDNA Homo sapiens cDNA clone Genexpress library idt: C; Genexpress_sequence_idt: ylc-22a07 Seq primer: (-21)MI3 universal. Location/Qualifiers 95277534 and F07318.1 c-22a07, mRNA sequence. Single read Genexpress-Genethon Contact: Genethon C. R. Acad. Sci. III, 7757816 Homo sapiens (human) its expression genexpress@genethon.fr /tissue_type="total brain" /dev_gtage="3 months old" /clome_lib="normalized infant brain cDNA" /note="Organ: brain; Vector: lafmid BA; Site_1: HindIII; /site_2: NotI; sex=Female; dev_stage=3 months old; isolate=muscular atrophy patient; tissue_type=total brain; total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the GI:672970 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="c-22a07" 'sex="Female" recherche Sci. Vie 318 (2), 263-272 (1995) ne sur le Genome Humain BP60 91002 EVRY Cedex, mRNA linear FRANCE EST 20-FEB-1995

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IMAGE: molecular integration of the analysis of the human gen
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1,rue de l'Internationale, BP60 91002 EVRY Cedex,
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/dev_stage="3 months old"
/clone lib="normalized infant brain cDNA"
/clone lib="normalized infant brain cDNA"
/clone lib="normalized infant brain; Site_1: HindIII;
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
/site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5; -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
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mol_type="mRNA"
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Genexpress-Genethon
Genethon Centre de recherche Bur le Genome Humain
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Homo sapiens (human)
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Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C.,
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Seq primer: (-21)M13_universal.
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IMAGE: molecular integration of the analysis of the human genome
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R. Acad. Sci. II
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/dev_stage="3 months old"
/clone lib="normalized infant brain cDNA"
/clone lib="normalized infant brain cDNA"
/clone lib="normalized infant brain cDNA"
/note="Organ: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
                                                                                            mRNA sequence.
                                                          GI:670049
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/db_xref="taxon:9606"
/clone="c-zoc01"
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/mol_type="mRNA"
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                                                                                                                 8 bp mRNA ]
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Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani Kabaktchis,C. and Tessier,A.
Sebastiani integration of the analysis of the human genome
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Seq_primer: (-21)MI3_universal.
Location/Qualifiers
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Genethon Centre de recherche sur le Genome Humain
1, rue de l'Internationale, BP60 91002 EVRY Cedex,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 33160778698
Human Genome Center, L-452
Lawrence Livermore National Laboratory
Livermore CA 94550
                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 357)
Ghiso, N.S., Eveleth, G.G., Lieuallen, K. and Lennon, G.G.
Infant brain cDNAs
Genomics 28 (3), 570-572 (1995)
                                                                                                                                                                                                                                                                                                                                                                        T26505 357 bp mRNA linear EST 15-Al AB282E2R Infant brain, LLNL array of Dr. M. Soares 1NIB Homo Bapiens cDNA clone LLAB282E2 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genethon
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                                                                                                                                                                                                                                                                 Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                 T26505.1 GI:773822
                                                                Contact: Greg G. Lennon
                                                                                       7490096
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/cotone lib="normalized infant brain cDNA"
/notes "Organ: brain; Vector: lafinid BA; Site 1: HindIII;
Site 2: NotI; sex=Female; dev_stage=3 months old;
isolate=muscular atrophy patient; tissue type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafinid BA vector. Clone library from B. Soares, Psychiatry
Dept. Columbia University, USA. Normalization_method:
Bento Soares, P.N.A.S in press"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="c-11e05"
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dev_stage="3 months old"
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Fax: 510 422 2282
Email: info@image.llnl.gov
                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
Insert Size: 2097
High quality sequence stops: 371 Source: IMAGE Consortium, LLNL
High quality sequence stops: 371 Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2097 Std Error: 0.00
Seq primer: M13RP1
Seq primer: M13RP1
High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 469)

Hillier,L., Clark,N., Dubuque,T.; Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R53330 469 bp mRNA linear EST 18-MAY-19983502.rl Soares infant brain 1NIB Homo sapiens CDMA clone IMAGE.39920 5' similar to gb:M23234 MULTIDRUG RESISTANCE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                       /organism="Homo sapiens"
/mol type="mRNA"
/db_xref="GDB:412461"
/db_xref="taxon:9606"
/clone="IMAGE:39920"
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/db_xref="taxon:9606"
/clone="LLAB282E2"
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mol_type="mRNA"
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/dev_stage="73 days post natal"
/lab_host="pH10B (ampicillin resistant)"
/clone_lib="Soares infant brain INIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not
                                                                                       /sex="female"
                                                                                                                                                                                                                                       ocation/Qualifiers
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BP220580 Sugano cDNA library,
COL03695, mRNA sequence.
BP220580
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1 (bases 1 to 568)

Suzuki,Y., Yamashita,R., Shirota,M., Sakakibara,Y., Chiba,J.,
Mizushima-Sugano,J., Nakai,K. and Sugano,S.

Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)
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HEP21483, mRNA sequence.
BP243819
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25; Conserva
                                                 BP220580.1 GI:52093485
                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan Email: yeuzukideme u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yutaka Suzuki
Department of Virology
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               sapiens (human)
sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="liver"
/cell_line="HepG2"
/clone_lib="Sugano_cDNA_library, liver_HepG2"
/note="hepatoma"
                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEP21483"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Homo sapiens"
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Pred. No. 0.99;
                                                                                             570 bp mu
orary, colon!
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                                                                                                Homo sapiens cDNA clone
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AG179058/c
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Matches 25
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 570)

Suzuki, Y. Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.
Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

LGenome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki

Contact: Yutaka Suzuki

Contact: Yutaka Suzuki

Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan

Email: ysuzuki@ins.u-tokyo.ac.jp.
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AG179058.1
GSS.
                                                                                                                                                                                                                                                 submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujiyama,A., Hattori,M., Toyoda,A., Totoki,Y., Watanabe,H. and Sakaki,Y. BAC end sequences of Library RPCI-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                        Sequencing: T7
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                                                                                                     Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-051D12.T7"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="COL03695"
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1. .570
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/clone_lib="Sugano cDNA library, colon'
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AG179442/c
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Ното вар
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Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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 sapiens ABCB1 gene,
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/cell_type="lymphocytes"
/clone_llb="RPCI-43 Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
/clone="RP43-051L12.T7"
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/clone_lib="RPCI-43 Chimpanzee Male
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: EcoRI
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Primates;
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Pred. No. 1;
3843 bp DNA linear GSS 15-DEC VIRTUAL TRANSCRIPT, partial sequence,
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                 GSS 15-DEC-2003
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VERSION
KEYWORDS
                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                     SOURCE
ORGANISM
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AY408955/c
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JOURNAL
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Query Match
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1 (bases 1 to 383)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M. A., Tanenbaum, D. M., Civello, D. R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Science 302 (5652), 1960-1963 (2003)
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                     2 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes ABCB1 gene, VIRTUAL TRANSCRIPT, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY408954.1 GI:39764922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence AY408955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY408955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan troglodytes (chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY408955.1 GI:39764923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14671302
Direct Submission
                                                                                                                                                                              Science 302 (5652), 1960-1963 (2003)
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                                                                                                                                                                                                                                    Inferring nonneutral evolution from human-chimp-mouse orthologous
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 9; Length 3843; ilarity 100.0%; Pred. No. 1.2; Conservative 0; Mismatches 0; Indels
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/locus_tag="HCM3396"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
'mol_type="genomic DNA"
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                                                                                                          Kejariwal, A.,
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BC042531/c
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                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 72 Row: 1 Column: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg, R.
Direct Submission
Submitted (02-JAN-2003) National Institutes of Health, Mammalian Submitted (02-JAN-2003) Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #CO42531 4035 bp π
Homo Bapiens, ATP-binding cassette,
4, clone IMAGE:4837724, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
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                                                                                                                                                                                                This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 9 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged,
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Nanavati,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BC042531
BC042531.1 GI:27503509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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                                                                                                                                                                                                                                                                                                                                                           Gibbs, R.A.
/tissue_type="Testis"
/clone_lib="NIH_MGC_97"
/lab_host="DH10B"
                                                                  /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4837724"
                                                                                                                                                                             Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
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                                                                                                                                  organism="Homo sapiens"
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/locus_tag="HCM3396"
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Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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RESULT 15
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Best Local S
Matches 24
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AV191114 AV191114 AV191114 AV191114 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk590b5 5', mRNA sequence. AV191114
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                                                                                                                                                                    1 CGAACCAGGCACGTGCAATGGCGA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp/, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes DNA, clone: RP43-051K11.T7, genomic survey
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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R.Site 2 : EcoRI.
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                                                                                                                                                                                                                                                                                      cell_type="lymphocytes"
clone_lib="RPCI-43 Chimpanzee
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                                                                                                                                                                                                                                                                                                                             sex="male"
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Search completed: February
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Unpublished (1999)
Contact: Yuji Kohara
Genome Blology Lab.
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                           1 CGAACCAGGGCACGTGCAATGGCGA 25
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Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (Dases 1 to 360)
Kohara,Y., Shin-i,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motohashi,T., Zeng,Q., Watanabe,H., Sugimoto,A.,
Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
Nomoto,H.
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hermaphrodite embryo"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AX522070 Sequence
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AX504329 25 bp DNA Sequence 32 from Patent WO0234291. AX504329 AX504329.1 GI:23386141	5; Conservative 0; Pred. No. 0.04; Similarity 100.0%; Pred. No. 0.04; S; Conservative 0; Mismatches 0; GCTTGTGATCCACGGACACTCCTAC 25	olgan, S.P. ompositions and methods for treating unltiple drug resistance ultiple drug resistance atent: WO 0234291-A 15 02-MAY-2002; atent: WO 0234291-A 15 02-MAY-2002; HB BRIGHAM AND WOMEN'S HOSPITAL, INC. Location/Qualifiers /organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	AX504312 25 bp DNA 1 Sequence 15 from Patent WO0234291. AX504312 1 GI:23386130 Homo Bapiens (human) Homo Bapiens Eukaryota; Metazoa; Chordata; Craniata; Vert	25 100.0 4646 6 CQ861565 25 100.0 4646 6 CQ861565 25 100.0 4646 6 AR380622 25 100.0 4646 6 AX336420 25 100.0 4646 6 AX335708 25 100.0 4646 6 AX335708 25 100.0 4646 6 AX395099 25 100.0 4646 6 AX594298 25 100.0 4646 9 HUMMDR1 25 100.0 4669 6 AR091275 25 100.0 4669 6 AR091275 25 100.0 4669 6 AR203322 25 100.0 4669 6 AR203322 25 100.0 4669 6 AR363344 25 100.0 8630 6 AR306491 25 100.0 8630 6 AR306492 25 100.0 8630 6 AR306492 25 100.0 98630 6 AR306492 25 100.0 9318 6 AR306492 25 100.0 93472 6 AX706975 25 100.0 98472 6 AX707905 25 100.0 98472 6 AX7079913 25 100.0 128993 6 AX7079913 25 100.0 128993 6 AX7079913 25 100.0 147436 2 AC079303
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SOURCE ORGANISM

Homo sapiens (human) Homo sapiens

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1 (bases 1 to 210)

Chen,C.J., Clark,D., Ueda,K., Pastan,I., Gottesman,M.M. and Roninson,I.B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Human multidrug resistant cell line
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RESULT 4
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BD171402/c
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BD171402 3843 bp
Method for predicting side effects
used therefor.
BD171402
BD171402.1 GI:28412692
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                                                                                                                                                                                                                                                                                                                                                                                                                               AX481416
Sequence 30 from Patent
AX481416
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Bhattnagar, S.K., George, A.L. Jr. and Nazarenko, I.
Amplification of nucleic acid sequences
Patent: US 5593840-A 1 14-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="unassigned DNA"
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Sequence 1 from Patent WO0192877.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3843)
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                                                25;
                                                                                                                                                            Sorrentino, B. and Schuetz, J.
Method of identifying and/or isolating stem
Patent: WO 0192877.A 1 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
Location/Qualifiers
                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GCTTGTGATCCACGGACACTCCTAC 25
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JP 200223769-A/1
13-AUG-2002
31-JAW-2001 JP 2001024723
ICHIRO IEIRI
C12N15/09,C12Q1/68,C12N15/00
Method for predicting side effects of primer used
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Pred. No. 0.047;
htive 0; Mismatches (
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RESULT 8 AX322789/c

> RESULT 10 AR452556/c

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PAT 20-FEB-2004

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Sequence 3 from Patent WO0192877.
AX322789
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Method of identifying and/or isolating stem cells
Patent: WO 0192877-A 3 06-DEC-2001;
ST. JUDE CHILDREN'S RESEARCH HOSPITAL (US)
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Mammalia; Eutheria; Primates;
1 (bases 1 to 3988)
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Phosphatidylcholine as a
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CC
FH Key
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             GCTTGTGATCCACGGACACTCCTAC 25
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06-AUG-1998 DE 198 35 526.2,15-DEC-1998
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pred. No. 0.047;
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Homo sapiens P-glycoprotein (
AF016535
AF016535.1 GI:2353263
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Sequence 1 from Patent DE19857750.
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Gottesman, M.M. and Roninson, I.B.
            Chen, C.J.,
                                                                         Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                           Stremmel, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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Stremmel, W.
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                                                                                                                                                                                                                                                           Similarity
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en,C.J., Chin,J.E., Ueda,K.,
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                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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Pred. No. 0.047;
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Pred. No. 0.047;
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          Clark, D.P.,
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            Pastan, I.,
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Chen.G., Duran.G.E., Steger,K.A., Lacayo,N.J., Jaffrezou,J.P.,
Dumontet,C. and Sikic,B.I.
Multidrug-resistant human sarcoma cells with a mutant
P-glycoprotein, altered phenotype, and resistance to cyclosporins
D.B. Biol. Chem. 272 (9), 5974-5982 (1997)
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Direct Submission
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87028230
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                                                                                             WIDKLYMVVGTIJAAI IHGAGLELMMLVEGEMTDI FANAGNLEDLMSNITNRSDINDTG
FFMNLEEDMTRYAYYYGGIGAGVLVAAY IQVSFWCLAAGRQIHKIRKQFFHAINRQBI
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FSVLIGAFSVGGASPSIEAFANAKGAAYEIFKIIDNKPSIDSYSKSGHKPDNIKGNLE
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'gene="mdr1"

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Sequence 5 from patent US 5830697.
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AR051650.1 GI:5975014
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Sikic, B.I. and Chen, G.
P-glycoprotein mutant resistant to cyclosporin modulation
Patent: US 5830697-A 1 03-NOV-1998;
Location/Qualifiers
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Sikic, B.I. and Chen, C.
P-glycoprotein mutant resistant to cyclosporin
Patent: US 5830697-A 5 03-NOV-1998;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Pred. No. 0.047;
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           Score 25; DB 6;
Pred. No. 0.047;
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SUNTORY LTD
OS Homo sapiens
PN JP 1990100680-A/1
PD 12-APR-1990
PF 05-OCT-1988 JP 19882:
PI UEDA KAZUMITSU, KOMAI
PC C12N15/12,C12N1/21,CC
CC strandedness: Single
CC topology: Linear;
CC *source: tissue_type:
CC *source: clone=SAM11.
FH Key
FT CDS 138.
FT CDS 138.
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1 (bases 1 to 4378)

Ueda, K. and Komano, T.

HUMAN NORMAL CELL-DERIVED MDR RELATED GENE

Patent: JP 1990100680-A 1 12-APR-1990;
                                                                       1 GCTTGTGATCCACGGACACTCCTAC 25
                                                                                                                                                                                                                                                                               mat_peptide
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E02326
E02326.1 GI:2170561
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                                                         GCTTGTGATCCACGGACACTCCTAC 2143
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JP 1990100680-A/1
12-APR-1990
05-OCT-1988 JP 1988251475
UEDA KAZUMITSU, KOMANO TORU
C12N15/12,C12N1/21,C12Q1/68;
                                                                                                             100.0%; 9 ilarity 100.0%; 1 Conservative 0;
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                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic RNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              tissue_type=Adrenal gland;
clone=SAM1132;
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                                                                                                                                                                                                                                                    /gene='Multidrug
/gene='MDRA1'
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relating
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138. .3980
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                 US-08-461-823-1
US-09-762-195-1
US-09-784-649A-5
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64.0	64.0	64.8	64.8		64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	64.8	66.4	66.4	66.4
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Sequence 26189, A	Sequence 6, Appli	Sequence 16688, A	Sequence 15043, A	Sequence 15042, A	Sequence 13903, A	Sequence 16897, A	Sequence 12820, A	Sequence 11533, A	Sequence 11651, A	Sequence 11783, A	Sequence 11705, A	Sequence 174876,	Sequence 174875,	Sequence 11850, A	Sequence 17556, A		Sequence 205912,

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Sequence

Query Match Best Local (

Similarity

100.0%; Score 25; DB 1; Length 2726; 100.0%; Pred. No. 0.019;

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CURRENT APPLICATION NUMBER: US/99/762,195

CURRENT FILING DATE: 2001-02-05

PRIOR APPLICATION NUMBER: PCT/EP99702426

PRIOR FILING DATE: 1999-08-06

PRIOR APPLICATION NUMBER: 198 35 526 2 DE
PRIOR FILING DATE: 1988-08-06

PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR APPLICATION NUMBER: 198 57 570.8 DE
PRIOR FILING DATE: 1998-12-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08784649A Patent No. 5830697 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1
LENGTH: 3988
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ORGANISM: Homo sapiens
-09-762-195-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Stremmel, Wolfgang
TITLE OF INVENTION: Protective Effect on Large Intestinal Mucosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equence 1, Application US/09762195 atent No. 6677319
                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: REG.NO. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sikic, Branimir I
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-GLYCOPROTEIN MUTANT RESISTANT TO
TITLE OF INVENTION: CYCLOSPORIN MODULATION
                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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STATE: CA
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1 Similarity 100.0%; Pred. No. 0.02;
25; Conservative 0; Mismatches
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                                                                                                                                                                         Version
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                                                                                Query Match
Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,649A
FILING DATE:
CLASSIFICATION: 435
CTASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: Reg.No. 5830697 36,677
REFERENCE/DOCKET NUMBER: 06037/007001
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                     TELEFAX: 415-854-0875
INFORMATION FOR SEQ ID NO:
                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 2200 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sikic, Bran
APPLICANT: Chen, Gang
TITLE OF INVENTION: P-
TITLE OF INVENTION: C)
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                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 4264 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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2168
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                                 1 GCTTGTGATCCACGGACACTCCTAC 25
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GCTTGTGATCCACGGACACTCCTAC 2144
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100.0%; Pred. No. 0.
ative 0; Mismatches
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                                                                                 100.0%;
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Pred. No. 0.0
0; Mismatches
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US-08-181-471-2/c
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US-08-181-471-2
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; Sequence 1167, Application US/09023655,
; Patent No. 6607879
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Best Local Similarity
Matches 25; Conserv
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APPLICANT: Lishko
APPLICANT: Lishko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                        APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: Jeffrey J. Seilhamer
APPLICANT: GOMPOSITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163 REFERENCE/DOCKET NUMBER: AN TELECOMMUNICATION INFORMATION: TELEPHONE: 619-792-3680
                                TITLE OF INVENTION: COTITLE OF INVENTION: EX NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U
ZIP: 92130
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STREET: 12526 High Bluff Drive, Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPOLOGY:
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                 ADDRESSEE:
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                                                                                                                                                INFORMATION:
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Lishko, Va
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3174 PORTER DRIVE
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METHOD FOR DELIVERING BENEFICIAL
COMPOSITIONS TO HAIR FOLLICLES
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                                                                                    THE DETECTION OF BLOOD CELL GENE
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US-09-023-655-1167
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US-08-752-447-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08752447 Patent No. 5994088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (650) 855-05
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE
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MEDIUM TYPE: Floppy
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                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,447
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                     ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mechetner APPLICANT: Roninson,
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les 25; Conserv
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CLASSIFICATION:
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                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
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NAME: NO. 5994088nan, Kev
REGISTRATION NUMBER: 35,3
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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300 South Wacker Drive, Seventh Floor
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100.0%; Pred. No. 0
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Methods and Reagents for Preparing
Using Immunoligcal Agents Specific
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                                   Kevin E
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TELEPHONE: 312-913-0001

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                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/752,447
APPLICATION NUMBER: 08/752,447
EILING DATE: 15-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6365357nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               equence 1, Application US/09316167
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APPLICANT: Mechet
APPLICANT: Ronins
                                                                                     TELEFAX: 312-913-9808 INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/316,167
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                     SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NITLE OF INVENTION: Wethods and Reagents for Preparing and PRITTLE OF INVENTION: Using Immunoligical Agents Specific for P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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TYPE: ... STRANDEDNESS: B1...
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LOCATION:
                                                                                                                                                                                                                                                                                  FILING DATE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANGEDNESS: single
                                                    ENGTH:
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                                   4669 base pairs
ucleic acid
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Roninson, Igor B
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Pred. No. 0.02;
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Query Match
Best Local Similarity
Matches 25; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09397233
Patent No. 6630327
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-397-233-1/c
                                                                                                                                                                                                                                                                          TELEFAX: 312-913-0002 INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/397,233
FILING DATE: 16-Sep-1999
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6630327nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95,1121-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                      FEATURE:
                                                                                                      FEATURE
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2454 GCTTGTGATCCACGGACACTCCTAC 2430
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                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Methods and Reagents for Preparing and Using Immunological Agents Specific for P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Mechetner, Eugene
Roninson, Igor B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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STATE: Illinois
                                     NAME/KEY:
                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 60606
                                                                                        NAME/KEY:
                                                                                                                                        NAME/KEY:
                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                         LENGTH: 4669 base pairs
                                                                                                                                                                                                                                                                                                          TELEPHONE: 312-913-0001
                                                                                                                      LOCATION:
                                                                    OCATION:
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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Query Match

100.0%; Score 25;

DB 4;

Length 4669;

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5206352-3/c
PATENT NO. 5206352
PATENT NO. 5206352
APPLICANT: RONINSON, IGOY B.; PASTAN ITA H.; GOTTESMAN,
MICHAEL M.
TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAININ
; SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN C
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA
; CURRENT APPLICATION DATA
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5206352-3/c
;Patent No. 5206352
,APPLICANT: Roninson,
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TITLE OF INVENTION: COMPOSITIONS FOR CLONES CONTAINING DNA
SEQUENCES ASSOCIATED WITH MULTIDRUG RESISTANCE IN HUMAN CELLS
NUMBER OF SEQUENCES: 4
CURRENT APPLICATION DATA:
                                                                                 RESULT 12
US-08-793-610-5/c
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Best Local Similarity
Matches 25; Conserv
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Matches
Sequence 5, Application US/08793610
Patent NO. 5858744
GENERAL INFORMATION:
APPLICANT: BAUM, Christopher
APPLICANT: STOCKING-HARBERS, Carol
                                                                                                                                                                                                                                                      Query Match
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FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 892,575
FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
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FILING DATE: 01-AUG-1986
APPLICATION NUMBER: 845,610
FILING DATE: 28-MAR-1986
                                                                                                                                                                                                                                      Local
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tive 0; Mismatches
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100.0%; Pred. No. 0.0
tive 0; Mismatches
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100.0%; Pred. No. 0.02;
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RESULT 13
US-09-306-417-1/c
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN PC-DOS/MS-DOS

SOFTWARE: PATENTIN PATA:

APPLICATION NUMBER: US/08/793,610

FILING DATE: 07-MAR-1997

PRIOR APPLICATION NUMBER: DE P 44 31 973.8

PILING DATE: 08-SEP-1994

PRIOR APPLICATION NUMBER: DE 194

PRIOR APPLICATION NUMBER: DE 195 03 952.1

FILING DATE: 07-FEB-1995

PRIOR APPLICATION NUMBER: DE 195 03 952.1

FILING DATE: 07-FEB-1995

PRIOR APPLICATION NUMBER: DE 195 03 952.1

PILING DATE: 07-FEB-1995

PRIOR APPLICATION NUMBER: DE 195 03 952.1

PILING DATE: 10-AUG-1995

APPLICATION NUMBER: DE 195 03 952.1

PRIOR APPLICATION NUMBER: 39.105

APPLICATION NUMBER: 39.105

REGISTRATION NUMBER: 39.105

REGISTRATION NUMBER: 39.105
                                                                                                                         EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09306417 Patent No. 6548301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
                                                                                                                                                                                                                           FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
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INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
OTHER INFORMATION: Description of Artificial Sequence: proviral
                          ORGANISM: Artificial Sequence FEATURE:
                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
                                                                                                    ENGTH: 8630
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OTHER INFORMATION: plasmid

DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 8630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09306417 Patent No. 6548301
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                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: P50491
                                                                                        NAME/KEY: misc feature
LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
                                                                              LOCATION: (1). (160)
OTHER INFORMATION: plasmid
                                                                                                                                                      OTHER INFORMATION: retroviral expression vector SFbeta91mSA1
                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: (1)..(8630)
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SFbeta71m4
                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: proviral OTHER INFORMATION: plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide
LOCATION: (1220)..(5062)
OTHER_INFORMATION: m4 mdr-1 cDNA
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LOCATION: (161)...(677)
OTHER INFORMATION: 5'-LTR
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LOCATION: (1) . (160)
OTHER INFORMATION: plasmid backbone
                                                                                                                                                                                                                                                                                     FEATURE:
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OTHER INFORMATION: plasmid backbone
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OTHER INFORMATION: 3'-LTR
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LOCATION: (5775)..(863
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LOCATION: (5215)..(577
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LOCATION: (532)..(1219)
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; OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2
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Best Local (
         INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 9318 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                       FILING DATE: 07-MAR-1997
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE P 4
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: DE 195
FILING DATE: 07-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/EP95/03175
APPLICATION NUMBER: PCT/EP95/03175
FILING DATE: 10-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Berman, Richard J.
REGISTRATION NUMBER: 39,105
REGISTRATION NUMBER: 39,105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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OTHER INFORMATION: 3'-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature LOCATION: (5215)..(577
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OTHER INFORMATION: mSA1 mdr1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: mat peptide LOCATION: (1220)..(50)
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LOCATION: (532)..(1219)
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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STRANDEDNESS:
                                                                                                       TELEPHONE:
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STOCKING-HARBERS, Carol
                                                                                     (202) 638-4810
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                                                                                                         (202) 638-5000
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100.0%; Pred. No. 0.02
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th Street N.W. Suite 330
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Title:
Perfect score:
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Maximum Match 10
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Maximum DB seq length: 200000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                    / Cgn2 6/ptodata/1/pubpna/US09E PUBCOMB.seq:*
/ Cgn2 6/ptodata/1/pubpna/US09C PUBCOMB.seq:*
/ Cgn2 6/ptodata/1/pubpna/US09C PUBCOMB.seq:*
/ Cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*
/ Cgn2 6/ptodata/1/pubpna/US10E PUBCOMB.seq:*
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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6/ptodata/1/pubpna/US10 NEW PUB.seq:*
6/ptodata/1/pubpna/US11_NEW PUB.seq:*
6/ptodata/1/pubpna/US60_NEW PUB.seq:*
6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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US-10-384-339C-30 US-09-866-866A-1 US-09-866-866A-3 US-09-805-020-30 US-10-072-621-2 US-10-097-340-1 US-10-007-926A-258 US-09-968-007A-459 US-09-968-007A-747 US-10-641-643-1167 US-10-343-657-1	D
Sequence 30, Appli Sequence 1, Appli Sequence 3, Appli Sequence 30, Appli Sequence 2, Appli Sequence 1, Appli Sequence 258, App Sequence 459, App Sequence 747, App Sequence 1167, App Sequence 11, Appli	Description

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1	-10-282-122A	-10-425-114-	US-10-425-114-13600	US-10-027-632-265708	027-632-	US-10-424-599-28742	-10-369-4	-10-282	US-09-938-842A-1088	US-09-938-842A-1088	US-10-027-632-36762	US-10-027-632-36762	7030	-7030	US-10-425-115-38049	US-10-101-510-127	US-10-227-646-161	US-09-860-670-161	-632	10177	-10-369-493-	2	US-10-027-632-126989	US-10-027-632-290365	US-10-027-632-290365	US-10-425-115-130740	US-09-801-274-269	US-10-619-359A-3	US-10-619-359A-1	US-10-101-433A-1	US-09-306-417-2	US-09-306-417-1	US-10-680-516-1	US-10-775-169-198
	Sequence 29808, A	Sequence 26722, A			26570	28/42	29334,	28884,	1088, A	7 '8801	e 36762	36762,	TOFO,	70301,	-	127, Ap	161,	161, /	e 101	Sequence 101776,		126989,		Sequence 290365,		130	N	e	, -	۳.		, -	. e	Sequence 198, App

ALIGNMENTS

RESULT 1 US-10-384-339C-30/c

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; SOFTWARE: PatentIn Ver. 2
; SEQ ID NO 30
; LENGTH: 3840
; TYPE: DNA
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/384,339C
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: PCT/EP02/00152
PRIOR PILING DATE: 2002-01-09
PRIOR PILING DATE: 2001-01-09
PRIOR APPLICATION NUMBER: DE 10155280.7
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR APPLICATION NUMBER: DE 10158411.3
PRIOR FILING DATE: 2001-10-26
                                                                                                                           US-10-384-339C-30
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Query Match 100.0%; Score 25; DB 18; Length 3840; Best Local Similarity 100.0%; Pred. No. 0.027; Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kreutzer, Roland
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING EXPRESSION OF A TARGET GE
FILE REFERENCE: 20200/2002
                                                                                                                                                       PUBLICATION INFORMATION:
TITLE: mdr-1
PATENT DOCUMENT NUMBER: AF016535
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: DE 10160151.4
PRIOR FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 173
SOFTWARE: Patentin Ver. 2.1
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Gaps

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GCTTGTGATCCACGGACACTCCTAC 25

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CURRENT APPLICATION NUMBER: US/09/866,866A
CURRENT FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: 09/584,586
PRIOR FILING DATE: 2000-05-31
PRIOR PILING DATE: 2000-05-31
PRIOR FILING DATE: 1990-05-27
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR APPLICATION NUMBER: 60/086,988
PRIOR FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
SOFTMARE: PACENTIN VETSION 3.0
SEQ ID NO 3
LENGTH: 3860
TYPE: DNA
ORGANISM: homo sapiens
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US-09-866-866A-3/c
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-866-866A-1
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US-09-866-866A-1/c
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PRIOR FILING DATE: 2000-05-31
PRIOR PELICATION NUMBER: PCT/US99/11825
PRIOR FILING DATE: 1999-05-27
PRIOR PAPPLICATION NUMBER: 60/086,988
PRIOR PILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Sorrentino, Brian
APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
                                                                                       Matches
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GENERAL INFORMATION:
                                                                                                         Query Match
Best Local Similarity
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APPLICANT: Schuetz, John
TITLE OF INVENTION: A Method of Identifying and/or Isolating Stem Cells
FILE REFERENCE: 1340-1-021CIP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watch 100.0%; Score 25; DB 9; Local Similarity 100.0%; Pred. No. 0.027; nes 25; Conservative 0; Mismatches
  2030
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                           GCTTGTGATCCACGGACACTCCTAC 25
  GCTTGTGATCCACGGACACTCCTAC 2006
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                                                                                       Conservative
                                                                                  100.0%; Score 25; DB 9;
100.0%; Pred. No. 0.027;
tive 0; Mismatches 0
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                                                                                                                            Length 3860;
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Sequence 30, Application US/09805020

Publication No. US2002086384A1

GENERAL INFORMATION:
APPLICANT: LEVINE, Zurit
TITLE OF INVENTION: SPLICE VARIANTS OF ONCOGENES
FILE REFERENCE: 2786-0168F
CURRENT APPLICATION UMBER: US/09/805,020
CURRENT FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 4533
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; ORGANISM: Homo sapiens
US-10-072-621-2
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US-09-805-020-30/c
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                                                                              Sequence 1, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 4643
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Best Local Similarity
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Best Local
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APPLICANT: Connop, Bruce P.
APPLICANT: Connop, Bruce P.
APPLICANT: Pollard, Michelle
TITLE OF INVENTION: REGULATION OF AMYLOID PRECURSOR PROTEIN EXPRESSION
TITLE OF INVENTION: BY MODIFICATION OF ABC TRANSPORTER EXPRESSION OR A
FILE REFERENCE: 100103.402
CURRENT APPLICATION NUMBER: US/10/072,621
CURRENT FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 10
APPLICANT:
                                        APPLICANT:
                                                               APPLICANT:
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                     Sebastian HOERSCH
Shubhangi KAMATKAR
Steve G. KOVATS
  Rachel E. MEYERS
                                                                                                                                                                                                                                                                                                                                                   Conservative
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Gordon B. MILLS Robert C. BAST, Jr

Peter VEIBY

Michael MORRISEY

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US-10-007-926A-258/c
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; ORGANISM: Homo Bapiens
US-10-097-340-1
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Best Local 9
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                                                                                                                PRIOR APPLICATION NUMBER: 60/254,090
PRIOR FILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 258, A Publication No.
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                    LENGTH: 4643
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR TRILING DATE: 2001-03-14
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CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
                                                                                                                                                                                                                        FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
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                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BERTUCCI, FRANCOIS
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPLICANT:
THER INFORMATION: atp-binding cassette, sub-family bother Information: (mdr/tap), member 1 (ABCB1) gene.
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FILING DATE: 2001-08-10
APPLICATION NUMBER: 60/325,102
FILING DATE: 2001-09-26
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FILING DATE: 2001/09/26
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BIRNBAUM, DANIEL
NGUYEN, CATHERINE
VIENS, PATRICE
FERT, VINCENT
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o. US20030143539A1
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Pred. No. 0.027;
Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                       Sequence 747, Application US/09968007A Publication No. US20040115625A1
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                                                                                                                                           TITLE OF INVENTION: Cancer Gene Determination and TITLE OF INVENTION: Gene Sets FILE REFERENCE: 689290-71 CURRENT APPLICATION NUMBER: US/09/968,007A CURRENT FILING DATE: 2001-10-02 PRIOR APPLICATION NUMBER: US/60/237,172 PRIOR FILING DATE: 2000-10-02 PRIOR FILING DATE: 2000-10-02
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 1001
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PRIOR APPLICATION NUMBER: US/60/237,173
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,278
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: US/60/237,294
PRIOR APPLICATION NUMBER: US/60/237,295
PRIOR APPLICATION NUMBER: US/60/237,295
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PRIOR FILING DATE: 2000-10-02
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TYPE: DNA
ORGANISM: Homo sapiens
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25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09968007A
o. US20040115625A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                    Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 25; DB 11;
Pred. No. 0.027;
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                                                                                                                                                                                                                                                                              Therapeutic Screening Usining Signa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 4643;
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SEQ ID NO 747

PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 1001 SOFTWARE: PatentIn version 3.0

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US-10-641-643-1167/c
, Sequence 1167, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 4646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                     US-10-641-643-1167
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Matches
                                                                   Matches
                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1167:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/10/641,643
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
PRIOR APPLICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                            CLONE: g187468
SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2454 GCTTGTGATCCACGGACACTCCTAC 2430
                                                                                                                                                                                                                                             IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cocks, Benjamin G.
1 GCTTGTGATCCACGGACACTCCTAC 25
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                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: PALO ALTO
                                                                                                                                                                                                                         LIBRARY: GENBANK
                                                                                                                                                                                                                                                                                                                                 LENGTH: 4646 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 11 llarity 100.0%; Pred. No. 0.027; Conservative 0; Mismatches
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                              E: (650) 855-05
(650) 845-4166
                                                                                      100.0%; Score 25; DB 17
100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENE EXPRESSION
                                                                                                                                                                              SEQ ID NO: 1167 :
                                                                   0
                                                                   Mismatches
                                                                                                          DB 17; Length 4646;
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                                                                   Indels
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RESULT 13 US-10-680-516-1/c

; Sequence 1, Application US/10680516; Publication No. US20040166110A1

GENERAL INFORMATION:

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US-10-775-169-198/c
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                                                                                                                                                        US-10-775-169-198
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Best Local S
Matches 25
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                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 5278
SOFTWARE: PatentIn version 3.2
SEQ ID NO 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 198, Application US/10775169
Publication No. US20040175743A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Routhson, Igor B.
APPLICANT: Routh, Adam
APPLICANT: Ruth, Adam
TITLE OF INVENTION: Mutations of the MDR1 P-glycoprotein that Improve Its
TITLE OF INVENTION: Ability to Confer Resistance to Chemotherapeutic Drugs
FILE REFERENCE: 00,616-A
CURRENT APPLICATION NUMBER: US/10/343,657
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: 60/222,313
PRIOR APPLICATION NUMBER: 60/222,313
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
                                                                          Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    APPLICANT: Twine, Natalie
APPLICANT: Dorner, Andrew
APPLICANT: Trepicchio, William
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
FILE REFERENCE: AMIDIO80 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wyeth
APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (425)..(4264)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 4646
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                              LENGTH: 4646
2454 GCTTGTGATCCACGGACACTCCTAC 2430
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                                    1 GCTTGTGATCCACGGACACTCCTAC
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                                                                          Conservative
                                                                                          100.0%; Score 25; 100.0%; Pred. No.
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                                                                          0; Mismatches
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Pred. No. 0.027;
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                                                                                                                  DB 18;
                                                                                              .027;
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                                                                                                                Length 4646;
                                                                            Indels
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RESULT 14
US-09-306-417-1/c
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        GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                         Sequence 1, Application US/09306417
Patent No. US20020103144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312-913-9808
INFORMATION FOR SEQ ID NO: 1:
OFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal
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APPLICATION NUMBER: US/10/680,516
FILING DATE: 07-Oct-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Noonan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/752,447 FILING DATE: 15-NOV-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roninson, Igor B
TITLE OF INVENTION: Methods and Reagents for Preparing and
Using Immunoligcal Agents Specific for P-glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: 3'UTR
LOCATION: 4265..4669
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: cDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Mechetner, Eugene
                                                                                                                                                                                                                                                                                                                                         2454 GCTTGTGATCCACGGACACTCCTAC 2430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        25;
                                                                                                                                                                                                                                                                                                                                                                              1 GCTTGTGATCCACGGACACTCCTAC 25
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STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                            n 100.0%; Score 25; DB 18; Length 4669; Similarity 100.0%; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4669 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff Ltd
STREET: 300 South Wacker Drive, Seventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHARACTERISTICS:
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425..4264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'UTR
1..424
                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95,1121
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US-09-306-417-2/c
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                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09306417 Patent No. US20020103144A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                               APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral Gene Transfer Vectors
FILE REFERENCE: P50491
CURRENT APPLICATION NUMBER: US/09/306,417
CURRENT FILING DATE: 1999-05-06
EARLIER APPLICATION NUMBER: DE 198 22 115
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)..(8630)
OTHER INFORMATION: retroviral expression vector SFbeta71m4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)..(160)
OTHER INFORMATION: plasmid backbone (pUC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: proviral OTHER INFORMATION: plasmid DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (5775)..(8630)
OTHER INFORMATION: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc_feature
LOCATION: (5215)..(5774)
OTHER INFORMATION: 3'-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (1220)...(5062)
OTHER INFORMATION: m4 mdr-1 cDNA
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LOCATION: (1220)..(50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (161)..(677)
OTHER INFORMATION: 5'-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature LOCATION: (161)..(677)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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                                                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: proviral OTHER INFORMATION: plasmid DNA
                                                                                                                                                                                                                      TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(160)
                                                        LOCATION: (1). (863
                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                           NAME/KEY: misc_feature
LOCATION: (1)..(8630)
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OTHER INFORMATION: plasmid backbone (pUC)
FEATURE:
NAME/KEY: misc feature
LOCATION: (1617. (677)
OTHER INFORMATION: 5'-LTR
FEATURE:
NAME/KEY: 5'UTR
LOCATION: (1219)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (1220). (5062)
OTHER INFORMATION: mSA1 mdr1 cDNA
FEATURE:
NAME/KEY: misc feature
LOCATION: (5215). (5774)
OTHER INFORMATION: 3'-LTR
FEATURE:
NAME/KEY: misc feature
LOCATION: (5775). (8630)
OTHER INFORMATION: plasmid backbone (pUC)
US-09-306-417-2

Query Match
Best Local Similarity 100.0%; Score 25; DB 9; Length 8630;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 25; Conservative 0; Mismatches 0; Gaps 0;

Query Match
LOCATION: (577GGATCCACGGACACTCCTAC 25
DB 3249 GCTTGTGATCCACGGACACTCCTAC 25
Search completed: February 9, 2005, 22:26:43
Job time: 267.667 secs
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Abg78185 Human MDR
Aaz49333 Human MDR
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ALIGNMENTS

RESULT 1 AAD39004

AAD39004 standard;

DNA; 25

ВP

AAD39004;

23-SEP-2002 (first entry)

Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy; polycythaemia vera; hypoxia responsive element; HRE; antisense; Human mdr1-HRE antisense oligonucleotide #7. 25-OCT-2001; 02-MAY-2002. Synthetic. Homo sapiens. WPI; 2002-471427/50. Colgan 26-OCT-2000; WO200234291-A2 modified_base phosphorothioate (BGHM) BRIGHAM & WOMENS HOSPITAL INC. 2000US-0243542P. 2001WO-US049856. Location/Qualifiers /*tag= a /mod_base= OTHER backbone; note= "Phosphorothioate backbone" 88.

Treating a subject (at risk of) having a hematologic malignancy or multidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia

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RESULT 2
AAD39014/c
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                         Treating a subject (at risk of) havi multidrug resistance, e.g. lymphoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiquitin-like-modifier; HIF-1; lymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; angiogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
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                                                                                                                       WPI; 2002-471427/50
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                                                                                                                                                                                                                                                   & WOMENS HOSPITAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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e.g. lymphoma or myeloma, by ad
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Matches
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The present invention relates to a standardized polynucleotide system, which comprises at least one carrier nucleic acid, at least 3 oligonucleotides, as primers and target-gecific, fluorescently labeled probe and optionally at least one set of stabilized controls (standard RNA or DNA) of known concentration and instructions. The system comprise any of 20 sets of one control, two primers and one target-specific probe
                                                                                                                                                                                                            Claim 1; Page 12; 38pp;
                                                                                                                                                                                                                                                                                                      Standardized polynucleotide system, useful for quantitative, determination of nucleic acid, comprises stabilized standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2002; 2002DE-01009071.
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RESULT 4
AAAC70907/c
ID AAQ70907 standard; DNA; 2726 BP
XX
AC AAQ70907;
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AC AAQ70907;
XX
POT 25-MAR-2003 (revised)
DT 27-MAR-1995 (first entry)
AC AAQ70907;
XX
Multidrug-resistance; MDR-1 gen
XX
Multidrug-resistance; MDR-1 gen
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Multidrug-resistance; MDR-1 gen
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Multidrug-resistance; MDR-1 gen
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POP MO9417206-A1.
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                                                                                                                                                                                                                                                                         This gene is used as an example of a target DNA in a method for the amplification of nucleic acid sequences in a mixture using various DNA probes/primers. The method may be used to detect a mutation or allele ithe target, e.g. that that causes a genetic disease. (Updated on 25-MAI 2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enzymatic amplification of target nucleic acid sequences in a mixt.detect a mutation or allele in the target, e.g. that causes a genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 30; 50pp; English
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Pred. No.
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                                                                                                       Score 25; DB 2; Length 2726; Pred. No. 0.081; Mismatches 0; Indels
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RESULT 5 AAQ70916/c

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RESULT 6
AAT43326
ID AAT433
XX AAT433
XX O1-SEP
XX DCR; p
XX PCR; p
XX LCR; h
XX LCR; h
XX Synthe
XX WO9639
PD 12-DEC
XX Y O4-JUN
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                                                                                                                                                                                                                                                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                modified copies -
or allele(s).
                                                                                                                                                                                                                                                                                                                                                                                                                                          Enzymatic amplification of target nucleic acid sequences to form exact or modified copies - has increased fidelity and can identify point mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1993;
16-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1994
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27-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bhatnagar SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JAN-1994;
                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 30; 69pp; English.
  05-JUN-1995;
                    04-JUN-1996;
                                                                                Synthetic.
                                                                                                                                 Multidrug resistance gene-1
                                                                                                                                                      01-SEP-1997
                                                                                                                                                                                             AAT43322 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ONCO-) ONCOR
                                         12-DEC-1996
                                                            WO9639537-A1
                                                                                                   primer;
human; m
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multidrug
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(first en
                                                                                                                                                      (first entry)
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93US-00168621.
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  95US-00461823
                      96WO-US008841
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resistance
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                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                Score 25;
Pred. No.
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                                                                                                    chain
gene;
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                                                                                                                                                                                                                                                                                                                               728 T;
                                                                                                     reaction; ligase chain reaction; MDR-1; ds.
                                                                                                                                                                                                                                                                                                 0.081;
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RESULT 7
ABV78146/c
ID ABV781
XX ABV781
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XX ID Human
XX RNA ir
KW Viruci
XX Homo E
XX H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the multidrug resistance gene (MDR-1) amplified CC by the primers shown in AAT43320 and AAT43321. This sequence can be used CC as a target nucleic acid (TNA) sequence contained in a nucleic acid or CC mixture of nucleic acid (TNA) sequence contained in a nucleic acid or CC mixture of nucleic acids while avoiding strand displacement by CC polymerase. The method comprises using three primers, one complementary. CC to a first segment of the TNA, a second complementary to a second segment composition of the first primer. And a third which is composition of the first primer. The first two primers are hybridised to the CC TNA, and a fused amplification product is created from the TNA using these two primers. The fused product is dissociated, and hybridised to the third primer, which is then extended. The extended modified CC these two primers are ligated. Each of the primers may be labelled using a CC thought of the product is hybridised to the first two primers, and these camplification product is product to the first the presence of a mutation or allele by detecting whether the labelled primer is CC contained within the fused amplification product or the extended camplification product. The method of the invention combines certain CC aspects of ligase chain reaction (LCR) and polymerase chain reaction (CC primers needed, and the fact that the entire TNA sequence does not need compared to LCR due to the reduced number of compared to LCR due to the reduced number of comparers and the fact that the entire TNA sequence does not need to be compared to LCR due to the reduced number of comparers and the fact that the entire TNA sequence does not need to be compared to LCR due to the reduced number of comparers to the compared to LCR due to the reduced number of comparers to the compared to LCR due to the reduced number of comparers to the compared to LCR due to the reduced number of comparers to the comparers to t
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Best Local S
Matches 25
                                 09-JAN-2001; 2001DE-01000586.
26-0CT-2001; 2001DE-01055280.
29-NOV-2001; 2001DE-01058411.
07-DEC-2001; 2001DE-01060151.
                                                                                                                                                                                                                                                                                                                             WO200255693-A2
                                                                                                                                                                                                09-JAN-2002; 2002WO-EP000152
                                                                                                                                                                                                                                                                18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mdr-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABV78146;
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                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                         virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-043158/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ition; dsRNA1; gene expression inhibitor; oncogene; cytostatic;
protozoacide; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 30.
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RESULT 8
ABZ35722/c
ID ABZ357
XX ABZ357
XX ABZ357
XX Double
KW Drotoz
KW Protoz
KW Protoz
KW Hepati
XX Homo 8
XX Homo 18
XX Inhibi
PT Hot the
XX Claim
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Matches
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Best Local
                           Inhibiting expression of target genes, useful by introducing into cells two double-stranded to the target.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to inhibiting expression of a target gene (I) in a cell by introducing an inhibitory RNA (dsRNA1) having a double-stranded structure of at most 49 consecutive bases. At least part of one strand (as1) of dsRNA1 is complementary to (I) and at least one end of dsRNA1 has an overhang of 1-4 nucleotides. The method is used to inhibit the expression of a wide range of genes, e.g. oncogenes, cytokine genes etc. in humans, also genes in Plasmodium or in viruses or viroids that are pathogenic for humans, animals or plants. Introducing an overhang into dsRNA greatly increases effectiveness for inhibiting gene expression, both in vivo and in vitro and also increases stability and thus the effective concentration inside the cell. The present sequence is that of
                                                                                                                                                                                                                                                                                                                            Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; protozoacide; gene expression; antisense; tumour; infection; I virus; viroid; anti-GFP; human; HIV; human immunodeficiency vi Hepatitis C virus; human papilloma virus; gene; ds.
                                                                                                                       Kreutzer
                                                                                                                                                                                                                                                                                                                                                                                                        Human mdr-1
                                                                                                                                                                                                                                                                                                                                                                                                                                       07-FEB-2003
                                                                                                                                                                                09-JAN-2001; 2001DE-01000588
                                                                                                                                                                                                            09-JAN-2001; 2001DE-01000588.
                                                                                                                                                                                                                                           18-JUL-2002
                                                                                                                                                                                                                                                                       DE10100588-A1.
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target and
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                                                                                                                                                    (RIBO-) RIBOPHARMA AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              having an overhang.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression of target gene, useful e.g. for inhibiting by administering double-stranded RNA complementary to
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide
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Pred. No.
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                                            for treating tumors,
that are complementa
                                              complementary
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                                                                                                                                                                                                                                                                                                                                                             Plasmodium;
                                                                                                                                                                                                                                                                                                                                                                           virucide;
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Claim 13; Page 27-28; 100pp; German

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The invention relates to inhibiting expression of a target gene in a cell CC by introducing at least two oligoribonucleotides (dsRNAI and II), both CC with a double-stranded (ds) structure of at most 49 sequential nucleotide CC pairs. At least part of one strand (S1, S2) of the ds structures in each CC of dsRNAI and II are complementary to regions in the target gene. The CC method uses antisense inhibition of gene expression using double stranded CC RNA inhibition (RNAi). The method is particularly used to treat tumours CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on CC of expression than known methods using a single dsRNA, even at very low CC concentrations. When dsRNA has at least one unpaired nucleotide at the CC end, stability (and thus effective concentration in the cell) is improved and efficiency can be increased further by pretreating the cells with CC interferon. The present sequence is that of a target DNA of the invention very
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                      This invention describes a novel method for inhibiting expression of a target gene by introducing into the cell that contains the target gene ileast one oligoribonucleotide (dsRNAI) that and double-stranded (ds) structure of not more than 49 consecutive nucleotides (nt), where at least a segment of one strand of the ds structure is complementary with the target gene and the cells are treated with interferon before introduction of dsRNAI. The method is used to inhibit expression of target genes, particularly oncogenes, cytokine genes, Id (not defined)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3840 BP; 1130 A; 738 C;
                                                                                                                                                                                                                                                                                Inhibiting expression of target genes, e.g. oncogenes, in cells, b introduction of complementary double-stranded oligoribonucleotide, treating the cell with interferon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human mdr-1
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  target genes, particularly oncogenes, cytokine genes, Id (not defined) protein genes; developmental or prion genes, or genes expressed in pathogenic organisms (particularly plasmodia) or in viruses or viroids (pathogenic in humans, animals or plants). Treating the cells with
                                                                                                                                                                                                                                            Disclosure; Page 32-33; 98pp; German
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-742209/81
                                                                                                                                                                                                                                                                                                                                                                                                           Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-2001; 2001DE-01000587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-2001; 2001DE-01000587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-NOV-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (RIBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibition; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIBOPHARMA AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTTGTGATCCACGGACACTCCTAC 2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCTTGTGATCCACGGACACTCCTAC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA fragment SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           Limmer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                           Rost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                           ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 6;
Pred. No. 0.083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    957 G;
                                                                                                                                                                                                                                                                                                                                                                                                           Hadwiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1015 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                             after
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GCTTGTGATCCACGGACACTCCTAC

Query Match Best Local S Matches 25

Similarity

100.0%; ilarity 100.0%; Conservative C

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Score 25; DB 6; Pred. No. 0.083;); Mismatches

6

Length 3840; Indels

0

Gaps

0

Sequence 3840

B₽;

1130 A; 738 C; 957 G;

1015 T; 0 U; 0 Other;

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RESULT 10
ABL91687/c
ID ABL916
XX ABL916
XX ABL916
XX ABL916
XX ABL916
XX Human
DE Human
XX Human
XX Human
XX Human
XX DE1010

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interferon greatly increases the extent to which dsRNA can inhibit expression of the target genes, and the effect is even greater when dsRNA are modified to increase their stability. ABX09936-ABX10075 represent gene fragments used to illustrate the method of the invention
                                               The invention relates to a method for inhibiting expression of a target gene (ABL91658-ABL91797) in a cell by introducing at least one oligoribonucleotide that has a double-stranded structure consisting of at most 49 sequential nucleotide pairs, with at least part of one strand complementary with the target gene and has at least part of one strand retranded segment of 1-4 nt. The method provides oligoribonucleotides for antisense inhibition of gene expression useful e.g. for treating tunours but the oligoribonucleotides may also be directed against genes present in pathogens (e.g. Plasmodium or viruses/viroids, pathogenic on humans, animals or plants) or against cytokine, Id, developmental or prion genes. The method provides more effective inhibition of gene expression than use of known oligonucleotides, probably because the unpaired overhang increases stability and thus intracellular concentration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3840 BP; 1130 A; 738 C; 957 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABL91687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL91687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 28-30; 104pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inhibiting gene expression in cells, useful for e.g. treating tumors, introducing double-stranded complementary oligoRNA having unpaired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kreutzer R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JAN-2001; 2001DE-01000586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JAN-2001; 2001DE-01000586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RIBO-) RIBOPHARMA AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲
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25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV; gene expression; oligoribonucleotide; tumour; pathogen;
virus; viroid; cytokine; prion; antisense oligonucleotide;
virucide; protozoacide; antibacterial; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Limmer S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA; 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hadwiger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 U; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 12
AAZ49332/c
ID AAZ493
XX AAZ493
AC AAZ493
XX II-MAI
XX II-MAI
XX DE Human
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ABQ78185/c
ID ABQ781
XX ABQ781
XX ABQ781
XX Human:
XX Human:
XX Homo s
XX Homo s
XX Homo s
XX Homo s
XX I SI CDS
FT CDS
FT Variat
FT AUG
FT AUG
XX JP2002
XX
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                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to presumption of the side effect of at least one immunosuppressant selected from tacrolimus and cyclosporin in which if the 267th base in the position of MDRI gene in the encoding region of the cDNA sequence is guanine, adenine or thymine, is investigated. The method is used for the presumption of the side effect of an immunosuppressant. The present sequence is that of the MDRI encoding cDNA immunosuppressant.
                              Human wild-type multidrug resistance-1 (MDR-1) cDNA.
                                                                                                                               AAZ49332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immunosuppressant; tacrolimus;
single nucleotide polymorphism; gene;
                                                                              14-MAR-2000
                                                                                                                                                                             AAZ49332 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3843 BP; 1129 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 6-11; 14pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Presuming the side effect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JAN-2001; 2001JP-00024723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human MDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ78185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SRLS-)
                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2027
                                                                                                                                                                                                                                                                                                    2030
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DB; ABB83950.
                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                    GCTTGTGATCCACGGACACTCCTAC 2006
                                                                                                                                                                                                                                                                                                                                     GCTTGTGATCCACGGACACTCCTAC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  즛
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          replace (2677, A/T)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "Single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "MDR1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25; DB 6;
Pred. No. 0.083;
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ss.
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cc resistance protein MDR-1. MDR-1 is a transmembrane efflux pump, cc responsible for the export of drugs from cells, particularly cancer cells. Wild-type MDR-1 shows increased resistance to etoposide and cc (AAY58187) where the Gly at position 185 is replaced by Val. The cinvention relates to transducing haematopoietic stem cells with nucleic cacid encoding an MDR protein and culturing the modified cells. The cmodified haematopoietic stem cells are useful in bone marrow transplantation (to reconstitute haematopoietic systems in patients who chave undergone chemotherapy or radiation therapy) and in ex vivo gene cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or cleukaemia. The modified cells can also be used to identify factors convolved in regulating proliferation and differentiation in haematopoietic stem cells. Haematopoietic stem cells that express MDR-1 cwill be protected against chemotherapeutic agents, so can be engrafted convolved in the patient is undergoing chemotherapy. Expansion of (rare) the modified cells provides sufficient cells to permit standard convolved in the patient is undergoing chemotherapy. Expansion of (rare) capansion of haematopoietic stem cells by at least 10-fold compared with a maximum of 4-fold in known procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents cDNA encoding human wild-type multidrug resistance protein MDR-1. MDR-1 is a transmembrane efflux pump,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 68-70; 113pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ex vivo expansion of hematopoietic stem cells transduced with a sequence encoding human multidrug resistance-1, used for bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sorrentino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens.
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/product= "Human wild-type MDR-1
/product= "553, .555, GTT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in AAZ49333"
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/note= "cDNA sequence of G185V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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2030 GCTTGTGATCCACGGACACTCCTAC

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GCTTGTGATCCACGGACACTCCTAC 25

Query Match Best Local (Matches

Similarity

100.0%;

Score 25; Pred. No. C; 957 G;

DB 3; 1022 ij,

Length 3860;

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U; 0 Other

Conservative

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Mismatches

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Gaps

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Sequence

3860

BP; 1135 A; 746

RESULT 13

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                                                                                                                                                                     CC resistance protein MDR-1, where the the Gly residue at postion 185 of the cefflux pump, responsible for the export of drugs from cells, particularly CC cancer cells. The wild-type MDR-1 shows increased resistance to etoposide and decreased resistance to vinca alkaloids compared with the G185V CC mutant. The invention relates to transducing haematopoietic stem cells CC with nucleic acid encoding an MDR protein and culturing the modified with nucleic acid encoding an MDR protein and culturing the modified CC cells. The modified haematopoietic stem cells are useful in bone marrow CC transplantation (to reconstitute haematopoietic systems in patients who CC have undergone chemotherapy or radiation therapy) and in ex vivo gene CC cells, e.g., thalassaemia, Gauchier's disease, sickle cell anaemia or CC leukaemia. The modified cells can also be used to identify factors CC involved in regulating proliferation and differentiation in haematopoietic stem cells that express MDR-1 CC will be protected against chemotherapeutic agents, so can be engrafted CC while the patient is undergoing chemotherapy. Expansion of (rare) thaematopoietic stem cells to permit standard CC biochemical analysis. Overexpression of MDR-1 allows cytokine-driven cCC expansion of haematopoietic stem cells by at least 10-fold compared with cCC a maximum of 4-fold in known procedures
                Query Match
Best Local Similarity
   Matches
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                                                                                                                              Sequence 3860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 79-82; 113pp; English.
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100.0%; ilarity 100.0%; Conservative 0
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                                                                                                                              BP;
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1. .3843
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                                                                                                                        1135 A; 746 C; 956 G;
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   Score 25; DB 3;
Pred. No. 0.083;
D; Mismatches 0
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      <u>,</u>
                                                                 Length 3860;
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                                                á
                                                                                                         Matches
                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                          The invention provides a method of identifying and/or isolating a stem cell that involves detecting the expression of an ATP transport protein containing a conserved ATP-binding cassette (BCRP) by a cell in a sample comprising stem cells. The isolated stem cells may be used in the treatment of diseases such as muscular dystrophy, degenerative liver disorder, myocardial infarction, Parkinson's disease, degenerative disorders of the brain, and for trissue regeneration or replacement. Haematopoietic cells can be used in bone marrow transplants (e.g., for treatment of leukemia) and for ex vivo gene therapy for treating blood diseases such as sickle cell anemia and thalassemia. The stem cells can also be used as cell targets in gene therapy protocols. The present sequence represents a sequence related to the BCRP for which no relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hepatotropic; n cardiant; gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BCRP DNA related seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a stem cell, for treating e.g., muscular dystrophy, myocardial infarction, Parkinson's disease, or neurodegenerative disorders, comprises detecting the expression of an ATP transport protein (BCRP) by a cell.
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29-MAY-2001;
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                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 53-55; 87pp; English.
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                                                                                                                                                                                                                                                                      information has been provided in the specification
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                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                       The invention provides a method of identifying and/or isolating a stem cell that involves detecting the expression of an AFP transport protein containing a conserved AFP-binding cassette (BCRP) by a cell in a sample comprising stem cells. The isolated stem cells may be used in the treatment of diseases such as muscular dystrophy, degenerative liver disorders of the brain, and for tissue regeneration or replacement. Haematopoietic cells can be used in bone marrow transplants (e.g., for treatment of leukemia) and for ex vivo gene therapy for treating blood diseases such as sickle cell anemia and thalassemia. The stem cells can also be used as cell targets in gene therapy protocols. The present seguence represents a seguence related to the BCRP for which no relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying a stem cell, for treating e.g., muscular dystrophy, myocardial infarction, Parkinson's disease, or neurodegenerative disorders, comprises detecting the expression of an ATP transport protein
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1 (bases 1 to 568)
Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J., Mizushima-Sugano, J., Nakai, K. and Sugano, S. Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions Genome Res. 14 (9), 1711-1718 (2004)
Contact: Yutaka Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP243819
BP243819 Sugano cDNA library,
HEP21483, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                        Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ime.u-tokyo.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
BP242809
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                                                                             GCTTGTGATCCACGGACACTCCTAC
                                                                                              GCTTGTGATCCACGGACACTCCTAC 25
                                                                                                                                            100.0%; Silarity 100.0%; F
Conservative 0;
                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol Type="mkNA"
/db xref="rtaxon:9606"
/clone="HEP21483"
/tissue type="liver"
/cell_line="HepG2"
/clone lib="Sugano cDNA library, l
/note="hepatoma"
                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                              Score 25;
Pred. No.
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cary, liver HepG2 Homo sapiens cDNA clone
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     linear
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      EST 15-SEP-2004
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FEATURES
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Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: ysuzuki@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                       2 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
                                  Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
                                                                                                                                                                                                                                                       Science 302 (5652), 1960-1963 (2003)
14671302
                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Terriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
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1 (bases 1 to 579)

Suzuki, Y., Yamashita, R., Shirota, M., Sakakibara, Y., Chiba, J.,
Mizushima-Sugano, J., Nakai, K. and Sugano, S.

Sequence comparison of human and mouse genes reveals a homologous
block structure in the promoter regions

Genome Res. 14 (9), 1711-1718 (2004)

Contact: Yutaka Suzuki
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BP242809
BP242809.1 GI:52115719
                                                                                             Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                     gene trios
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic survey sequence
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/db_xref="taxon:9606"
/clone="HEP17994"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="liver"
/cell_line="HepG2"
/coln_lin="Sugano cDNA library, liver HepG2"
/note="hepatoma"
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|mol_type="mRNA"
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100.0%; Pred. No. 0.56;
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VIRTUAL TRANSCRIPT, partial sequence,
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8X645450 497 bp
DKFZp781C1343_r1 781 (synonym: h
DKFZp781C1343_5', mRNA sequence.
                                                                                                                                                                                               25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 3843)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
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AY408955
AY408955.1 GI:39764923
GSS.
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3843 bp DNA linear GSS 15-DEC-2003
Pan troglodytes ABCB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-2003) Celera Genomics, Rockville, MD 20850, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                       /gene="ABCB1"
                                                                                                                                                                                                                                                                                                                                                                        organism="Pan troglodytes"/
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                                                                                                                                                                                                            100.0%; Score 25; DB 9
100.0%; Pred. No. 0.63;
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                    bp mRNA
m: hlcc4) Homo
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DEFINITION

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Best Local
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                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wellenreuther, R.,
Unpublished (2003)
Contact: MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)

Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                  534 bp mRNA linear EST 01-JAN-EST01407 Atlantic salmon Lambda Zap Express ovary cDNA library Salmo salar cDNA clone oyr_004_d08 5', mXNA sequence.
BM414475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No s1 sequence available.
This clone (DKFZp781C1343) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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BX645450.1
Contact: Caplice NC
Department of Microbiology
National University of Ireland Galway (NUIG)
National University of Ireland Galway, Galway
Tel: 00353 91 524411 2254
Fax: 00353 91 525700
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo. 1 (bases 1 to 534) S. Davey, G.C. and Powell, R. Caplice, N.C., Martin, S.A., Davey, G.C. and Powell, R. An expressed sequence tag-based list of genes expressed in the testis and ovary of Atlantic salmon (Salmo salar)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           German Genome Project
                                                                                                                                                                                                                                                                                                   Salmo salar
                                                                                                                                                                                                                                                                                                                                                               BM414475.1 GI:40542222
                                                                                                                           Unpublished (2002)
                                                                                                                                                                                                                                                                                                                     Salmo salar (Atlantic salmon)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="781 (synonym: hlcc4)"
/note="Vector: pSport1_Sfi; Site_1: SfiIA; Site_2: SfiIB; cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="DKFZp781C1343"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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100.0%; Pred. No.
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REFERENCE
AUTHORS
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BX317766/c
                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                TITLE
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Plate: ovary rare plate 4 row: d column: 08
Seq primer: M13 reverse primer = caggaaacagctatgacc
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                                                                                                                                                                                                                                                                             On Apr 7, 2003 tnis
Contact: Guiguen Y
INRA - SCRIBE
                                                                                                                                                                                                                                                                                                                            Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29598411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
22; Conserv
                                                                                                                                              Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and re
at sigenasupport@jouy.inra.fr to obtain the
                                                                                                                                                                                                                  Campus de beaulieu,
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oncorhynchus mykiss
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                                                                               primer: M13F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   was constructed using the Lambda Zap Express/Gigapack cloning kit (Stratagene cloning systems). CDNA synthesis was carried out using an oligo (dT) primer for the reverse transcription of 5ug of mRNA and the library was constructed by directional cloning EcoR1-Xho1 based on manufacturers instructions. An insert:vector ligation ratio of 1:5 was chosen as most optimum. The lambda library was packaged with Gigapack III gold packaging extracts and plated on the E. coli cell line XLI-Blue
1. .569
/organism="Oncorhynchus mykiss"
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EcoR1; Site_2: Xho1; An Atlantic salmon ovary cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8030"
/clone="oyr_004_d08"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Salmo salar"
/mol_type="mRNA"
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/dev_stage="adult"
/clone_lib="Atlantic salmon Lambda Zap Express ovary cDNA
                                                        Location/Qualifiers
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91.7%;
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Pred. No. 56;
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                                                                                                                                                        repetitions. Contact us 
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RESULT 8
BX320207/c
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Govoroun, M., Guiguen, Y. and Le Gac, F.
Govoroun, M., Guiguen, Y. and Le Gac, F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
On Apr 7, 2003 this sequence version replaced gi:29600852.
Contact: Guiguen Y
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Sequence cleaned of vector, adaptator and re
at sigenasupport@jouy.inra.fr to obtain the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Campus de beaulieu, RENNES cedex,
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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BX320207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 0038
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                                                                                                                                                                                                                                                                                                                                                                                                                      primer: Ml3F.
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                                                                                                                                /tissue_type="adipose tissue, blood, brain, differentiating gonads, gills, interrenal, intestine, kidney, liver, muscle, ovary, pituitary, testis" /dev stage="from embryos to adults" /lab_host="DH10B"
/clone lib="tcay"
/note="Vector: pT713D-pac; Rainbow trout multi-tissues
normalized + 1 subtraction (tcay); Clone distribution
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
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/clone lib="tcay"
/note="Vector: pT7T3D-pac; Rainbow trout multi-tissues
normalized + 1 subtraction (tcay); Clone distribution
AGENAE Resource centre. Francois PIUMI,
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/tissue_type="adipose tissue, blood, brain,
differentiating gonads, gills, interrenal, intestine,
kidney, liver, muscle, ovary, pituitary, testis"
/dev_stage="from embryos to adults"
/lab host="phi08"
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                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:8022"
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                                                                                                                                                                                                                                                                      clone="tcay0038b.a.22"
                                                                                                                                                                                                                                                                                                                                           organism="Oncorhynchus mykiss"
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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0; Mismatches
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Pred. No. 5
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REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

ACCESSION VERSION

KEYWORDS

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Matches

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RESULT 10
CA044923/c
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bkoop@wic.ca
Genome Sciences Centre, BC Cancer Agency
Genome Sciences Centre, BC Cancer Agency
CDNA preparation, sequencing and bioinformatics:
CDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Girn, R Guin, D Le
S Lee, T Olson, P Pandoh, A Prahbu, D Smailus, L Spence, J
S Taylor, G Yang, J Schein, S Jones and M Marra.
Location/Qualifiers
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ssalmge003036 gut Salmo salar
CA044923
CA044923.1 GI:24349786
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University of Victoria
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A survey of Salmo salar transcripts from high complexity cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 250 472 4067 Fax: 250 472 4075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Koop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PO Box 3020 STN CSC,
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/clone lib="mixed_tissue"
/note="Vector: pCMVsport6; Library Creator: Research
/note="Vector: pCMVsport6; Library Creator: Carlo
Genetics; Atlantic Salmon tissue contributors: Carlo
Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.)
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Salmo salar"
/mol_type="mRNA"
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strain="McConnell"
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Pred. No. 56;
0; Mismatches
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bkoop@uvic.ca
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria
CDNA preparation and sequencing:
CDNA preparation and sequencing:
Roberto Alberto, Marianne Beetz-Sargent, Maura Busby,
Roberto Hunt. Linda McKinnel, BF Koop.
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Salmo salar (Atlantic salmon)
Salmo salar
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University of Victoria
PO Box 3020 STN CSC, Victoria BC,
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1 (bases 1 to 592)
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http://web.uvic.ca/cbr/grasp.
                                                                                                                                                                                                                                                                                                                                                                                       mKNA sequence.
BX910867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 250 472 4067
Fax: 250 472 4075
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                                                                                                                                                             Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

1 (bases 1 to 595)
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                                                                                                                     Unpublished (2003)
On Jan 22, 2004 this sequence version replaced gi:41127666
                                                                                                                                                                                                                                                                                                        Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
                   Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                             Campus de beaulieu,
                                                                                 Contact: Guiguen
INRA - SCRIBE
                                                                                                                                                                                                                                                                                                                                                                      BX910867.2 GI:43415782
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Yann.Guiguen@beaulieu.rennes.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:8030"
/clone_lib="gut"
/clone_lib="gut"
/clone_lib="gut"
/clone="Vector: pBlueScriptIISK+; Library Creator: Matthe / Note="Vector: pBlueScriptIISK+; Library Creator: Matthe L Rise; Atlantic salmon tissue contributors: Carlo Biagi L Rise; Atlantic salmon tissue contributors: Carlo Biagi L Rise; Atlantic salmon tissue contributors: Carlo Biagi L Rise; Atlantic Salmon tissue contributors: Mattheway (Crofton, Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery (Crofton, B.C.), Rachel Roper (University of Victoria)"
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/strain="McConnell"
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91.7%;
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                                                                                                                                                                                                                                                                                                                         Contact: Guiguen Y
INRA - SCRIBE
Campus de beaulieu, I
Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
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Seq primer: M13R.
                                                                                                                                                                                                                                                        Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2003)
On Dec 17, 2003 this sequence version replaced gi:39992052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Govoroun,M., Guiguen,Y. and Le Gac,F.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="tcbk0072c.m.23"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
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                                        /clone="tcba0027c.l.14"
/tissue_type="multi-tissues"
                                                                                   /organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
                                                                                                                                                                       Location/Qualifiers
dev_stage="from embryos to adults"
lab_host="DH108"
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Pred. No. 56;
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tcba0027c.l.14 5prim,
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centre for Biomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC,
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ssalrgb531310 mixed_tissue Salmo
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Genome Sciences Centre,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 250 472 4067
Fax: 250 472 4075
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A survey of Salmo salar transcripts from high complexity cDNA
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Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Proteacanthopterygii; Salmoniformes; Salmonidae; Salmo.
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/clone lib="mixed tissue"
/clone lib="mixed tissue"
/note="Vector: pcWVsport6; Library Creator: Research
Genetics; Atlantic salmon tissue contributors: Carlo
Biagi, Mitch Uh and Robert Devlin (DFO, Vancouver, B.C.),
Simon Jones (PBS, Nanaimo, B.C.), Seaspring Hatchery
(Crofton, B.C.), Rachel Roper (University of Victoria)"
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Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
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/mol_type="mRNA"
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91.7%;
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Salmo salar
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Contact: Koop BF
                    Unpublished (2002)
                                                        http://web.uvic.ca/cbr/grasp
A survey of Salmo salar trans
                                                                                           GRASP Consortium, Davidson, W.S., Koop, B.F. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Yann.Guiguen@beaulieu.rennes.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact
at sigenasupport@jouy.inra.fr to obtain the chromatogram of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 02.23.48.50.09
Fax: 02.23.48.50.20
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Construction and primary characterization of normalized cDNA
Libraries in rainbow trout, Oncorhynchus mykiss
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Oncorhynchus mykiss
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INRA - SCRIBE
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Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"
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/lab_host="DH10B"
/clore 114
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/mol_type="mRNA"
/db xref="taxon:8022"
/clone="tcbi0021c.n.22"
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Pred. No. 56;
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University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Pol: 250 472 4067
Fax: 250 472 4075
Email: bkoop@uvic.ca
Genome Sciences Centre, BC Cancer Agency cDNA preparation,
Bequencing and bioinformatics: Y Butterfield, R Kirkpatrick, J
Bequencing and bioinformatics: Siee, Tolson, P Bandoh, A Prahbu, D
Smailus, L Spence, J Stott, S Taylor, G Yang, J Schein, S Jones and
M Marra.
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